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**United States Patent** [19]

Maruta et al.

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[54] **RECOMBINANT THERMOSTABLE ENZYME WHICH FORMS NON-REDUCING SACCHARIDE FROM REDUCING AMYLACEOUS SACCHARIDE**

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**[30] Foreign Application Priority Data**

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Jul. 4, 1995 [JP] Japan ..... 7-189706

[51] **Int. Cl.<sup>6</sup>** ..... **C12P 19/18; C12P 19/16; C12P 19/14; C12N 9/26**

[52] **U.S. Cl.** ..... **435/97; 435/96; 435/99; 435/101; 435/200; 435/201; 435/202; 435/205**

[58] **Field of Search** ..... 435/97, 99, 96, 435/101, 200, 201, 202, 205

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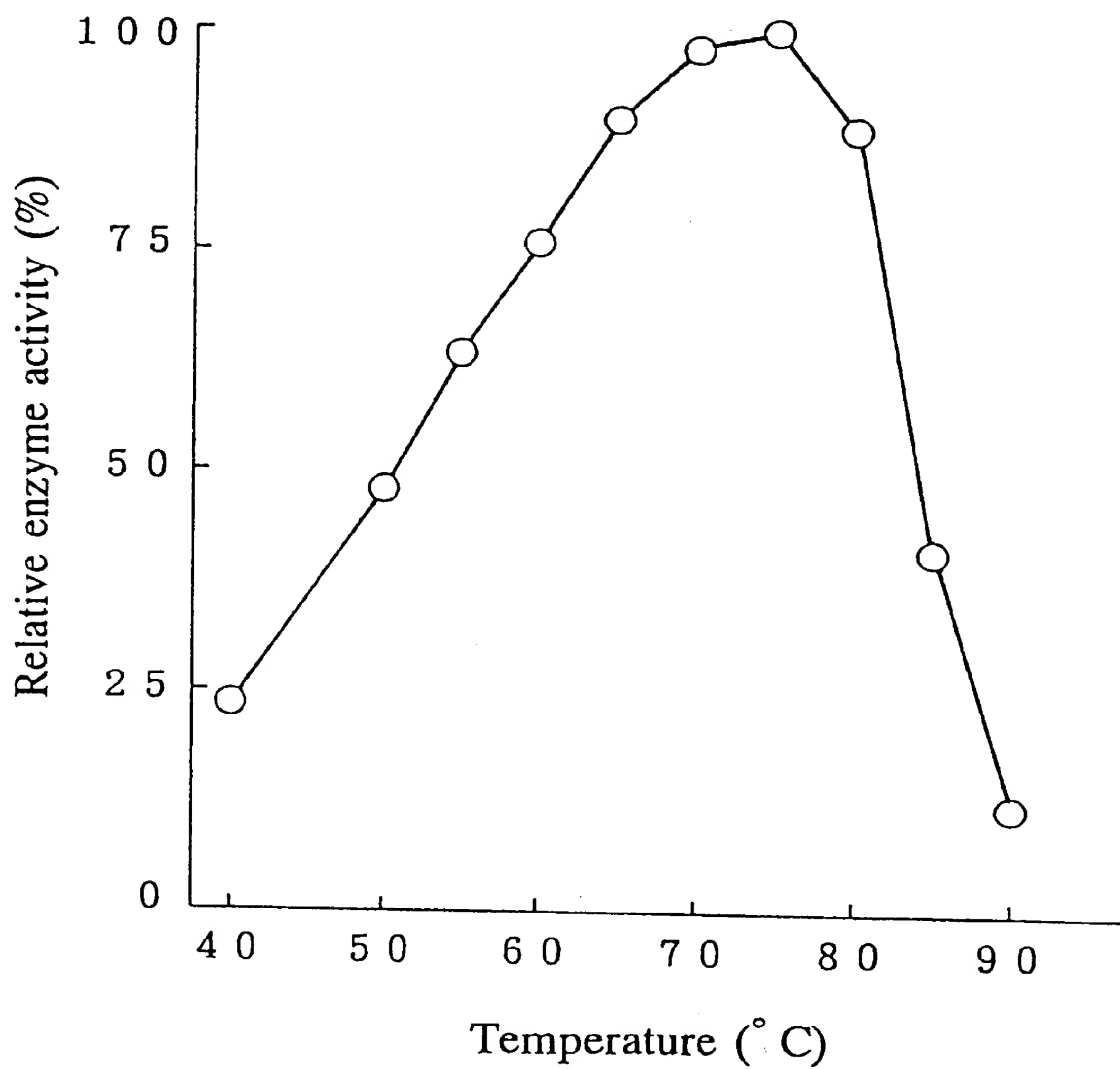
*Primary Examiner*—Rebecca E. Prouty

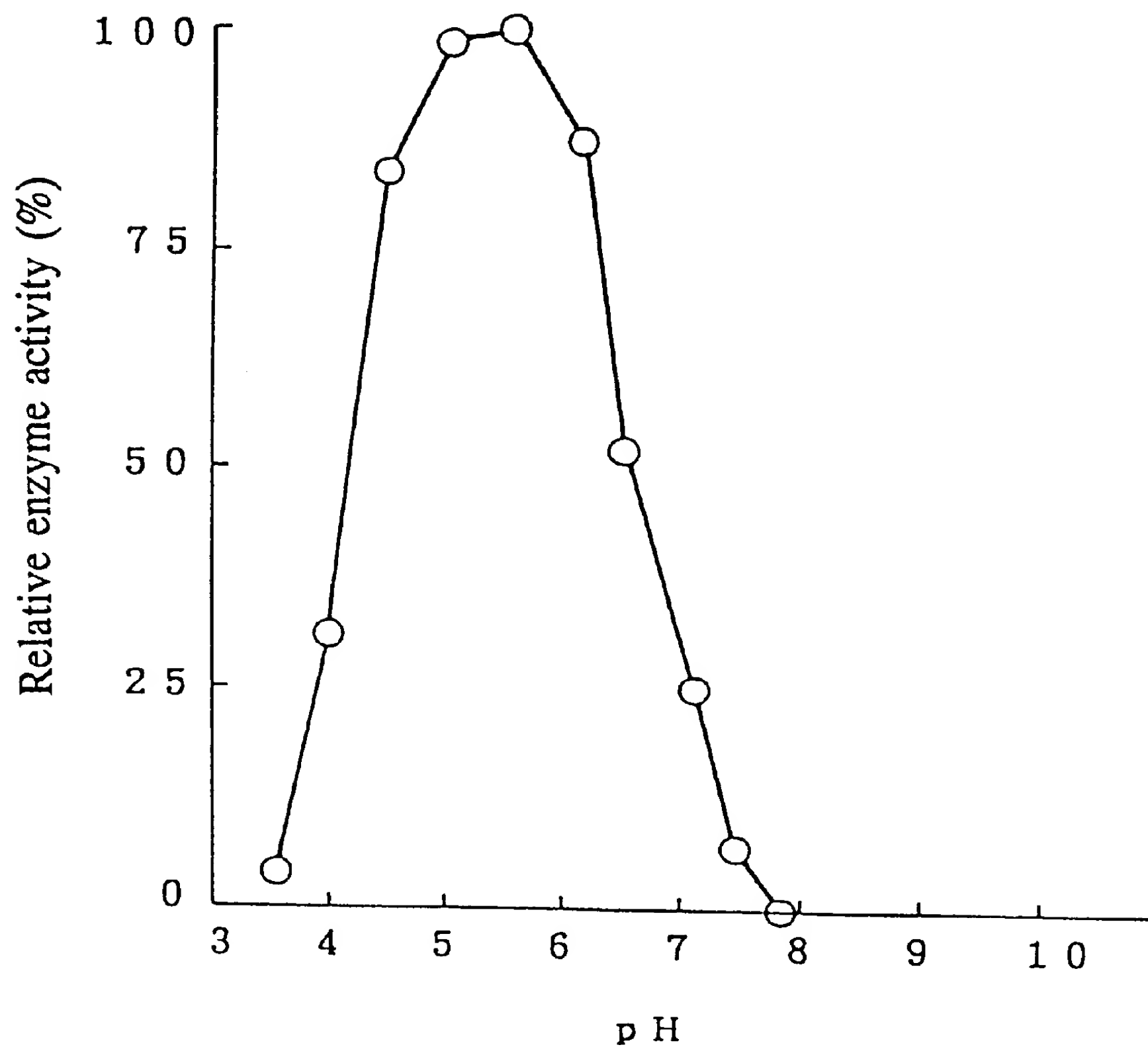
*Attorney, Agent, or Firm*—Browdy and Neimark

**[57] ABSTRACT**

Disclosed is a recombinant thermostable enzyme which has a molecular weight of about 69,000–79,000 daltons and a pI of about 5.4–6.4, and forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3. The enzyme has satisfactorily high thermostability, i.e. it is substantially not inactivated even when incubated in an aqueous solution (pH 7.0) at 85° C. for 60 min, and this facilitates the production of such non-reducing saccharides on an industrial scale and in a satisfactorily-high yield.

**7 Claims, 6 Drawing Sheets**

**FIG.1**

**FIG.2**

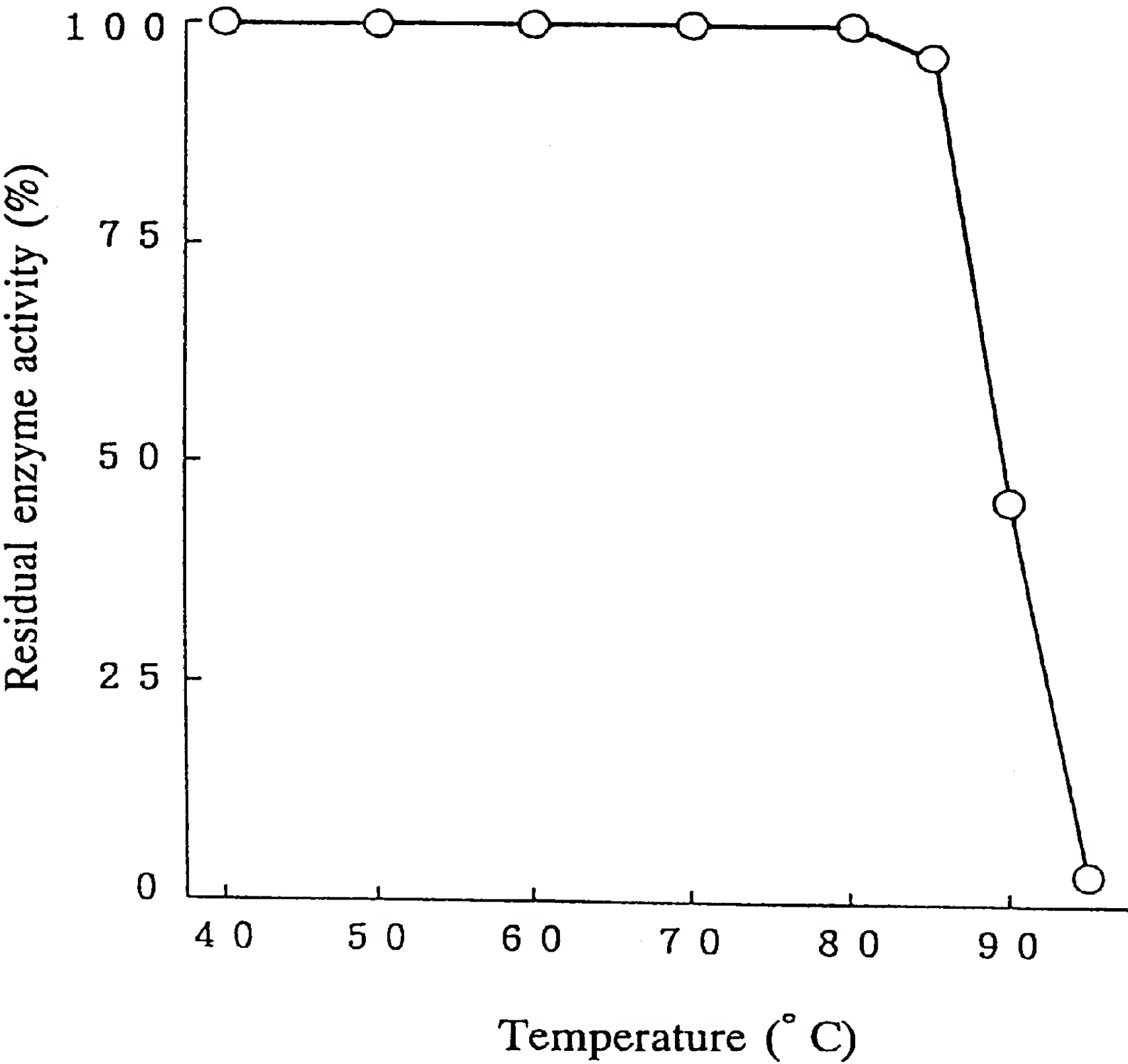


FIG.3

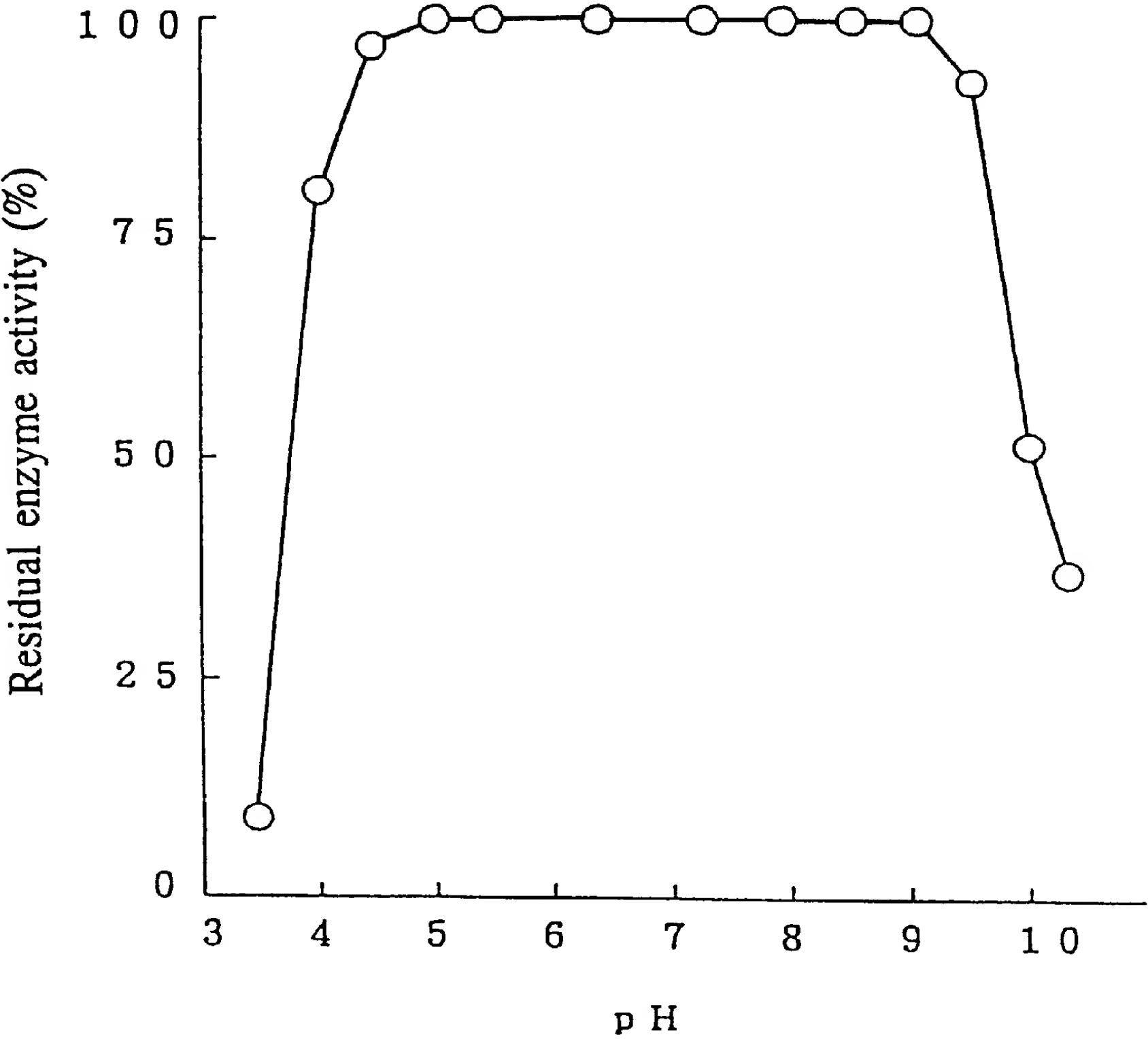


FIG.4

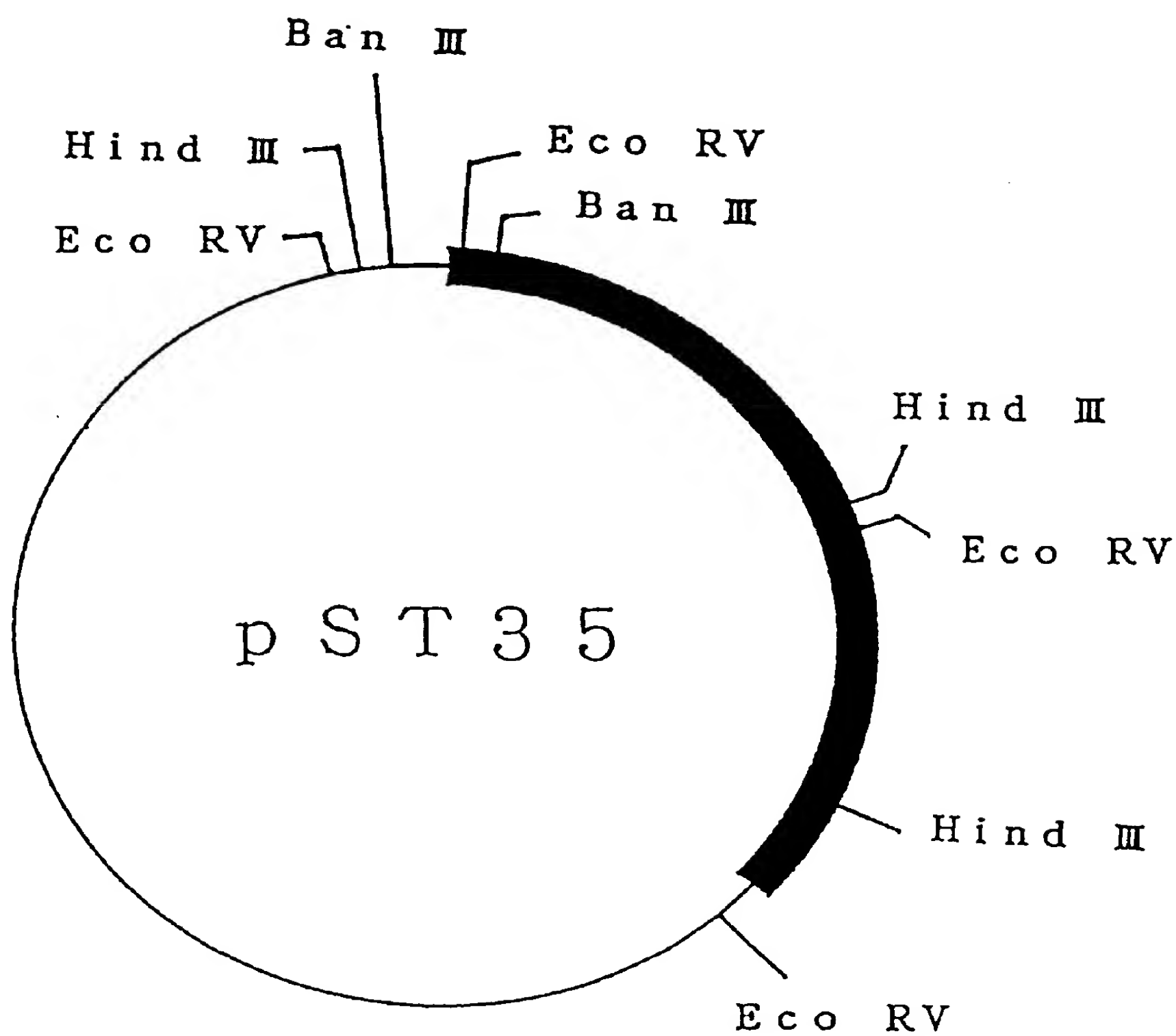


FIG.5

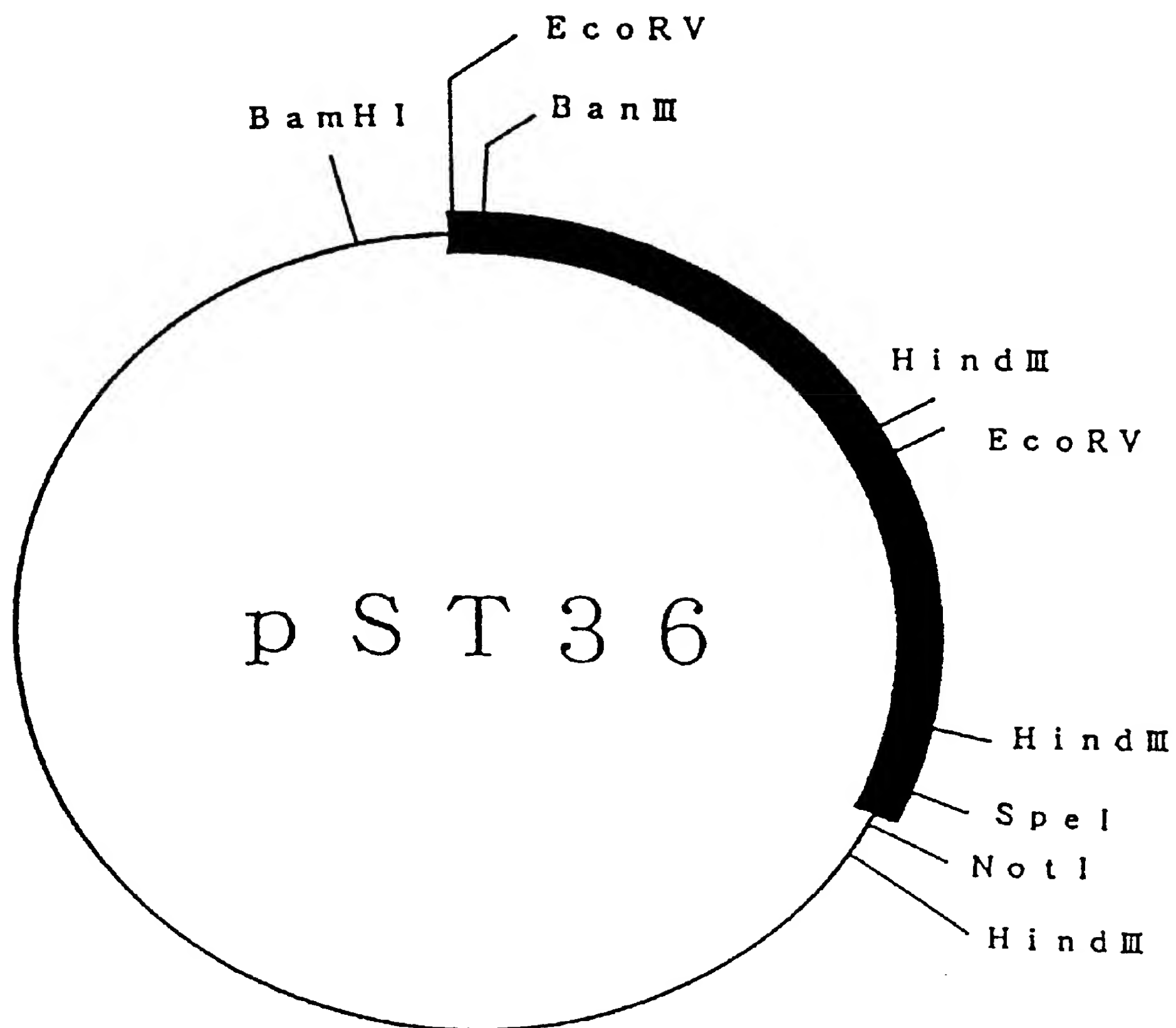


FIG.6

# RECOMBINANT THERMOSTABLE ENZYME WHICH FORMS NON-REDUCING SACCHARIDE FROM REDUCING AMYLACEOUS SACCHARIDE

## CROSS-REFERENCE TO RELATED APPLICATIONS

The present application is a division of parent application Ser. No. 08/505,448, filed Jul. 21, 1995.

## BACKGROUND OF THE INVENTION

### 1. Field of the Invention

The present invention relates to a recombinant enzyme which forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3.

### 2. Description of the Prior Art

Trehalose is a disaccharide which consists of 2 glucose molecules that are linked together with their reducing groups, and, naturally, it is present in fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can advantageously sweeten food products without fear of causing unsatisfactory coloration and deterioration. Trehalose, however, could not have been readily prepared in a desired amount by conventional production methods, so that it has not scarcely been used for sweetening food products.

Conventional production methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other using a multi-enzymatic system where several enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No. 154,485/75, is a method which comprises growing microorganisms such as bacteria and yeasts in nutrient culture media, and collecting trehalose mainly from the proliferated cells. The latter, as disclosed in Japanese Patent Laid-Open No. 216,695/83, is a method which comprises providing maltose as a substrate, allowing a multi-enzymatic system using maltose- and trehalose-phosphorylases to act on maltose, and recovering the formed trehalose from the reaction system. The former facilitates the growth of microorganisms, but has a demerit that the content in the microorganisms is at most 15 w/w %, on a dry solid basis (d.s.b.). Although the latter can readily separate trehalose, it is theoretically difficult to increase the trehalose yield by allowing such enzymes to act on substrates at a considerably-high concentration because the enzymatic reaction in itself is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

In view of the foregoing, the present inventors energetically screened enzymes which form non-reducing saccharides having a trehalose structure from amylaceous saccharides having a degree of glucose polymerization of at least 3, and have found that microorganisms such as those of the genera *Rhizobium* and *Arthrobacter* produce an absolutely novel enzyme which forms such non-reducing saccharides from such reducing amylaceous saccharides. They disclosed such an enzyme in Japanese Patent Application No. 349,216/93. They also found that trehalose is readily formed from such non-reducing saccharides when glucoamylase or  $\alpha$ -glucosidase acts on them.

It was found that the enzymes produced from the aforesaid microorganisms have an optimum temperature of about

40° C., and have some difficulties in their thermostability when used to prepare trehalose. It is recognized in this field that the recommendable temperature in the saccharification reaction of starch or amylaceous saccharides is one which exceeds 55° C. because the contamination of microorganisms will occur at a temperature of 55° C. or lower, decrease the pH of the reaction mixtures, and inactivate the enzymes used. Thus, a relatively-large amount of substrates remain intact. While the use of enzymes with a poor thermostability, a great care should be taken to control the pH, and, when the pH level lowers to extremely low level, alkalis should be added to reaction mixtures to increase the pH level as quickly as possible.

In view of the foregoing, the present inventors screened thermostable enzyme with such a novel enzyme activity and have found that enzymes produced from microorganisms of the genus *Sulfolobus* including *Sulfolobus acidocaldarius* (ATCC 33909) are not substantially inactivated even when incubated at a temperature exceeding 55° C., and they efficiently produce such non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides. These micro-organisms, however, are not sufficient in the enzyme productivity, and this requires a relatively-large scale culture to industrially produce non-reducing saccharides having a trehalose structure as an end unit.

Recently, the recombinant DNA technology has made a remarkable progress. At present, even an enzyme whose total amino acid sequence has not been revealed can be readily prepared in a desired amount, if once a gene encoding the enzyme is isolated and the base sequence is decoded, by preparing a recombinant DNA containing a DNA that encodes the enzyme, introducing the recombinant DNA into microorganisms or cells of plants or animals, and culturing the resultant transformants. Under these circumstances, urgently required are to find a gene that encodes the thermostable enzyme and to decode the base sequence.

## SUMMARY OF THE INVENTION

It is an object of the present invention to provide a recombinant thermostable enzyme which forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides with a degree of glucose polymerization of at least 3 by using the recombinant DNA technology.

It is a further object of the present invention to provide a DNA which encodes the recombinant thermostable enzyme.

It is yet another object of the present invention to provide a replicable recombinant DNA which contains the DNA.

It is another object of the present invention to provide a transformant into which the recombinant DNA is introduced.

It is yet another object of the present invention to provide a process for preparing the recombinant thermostable enzyme using the transformant.

It is another object of the present invention to provide a method for converting reducing amylaceous saccharides with a degree of glucose polymerization of at least 3 into non-reducing saccharides having a trehalose structure as an end unit.

The first object of the present invention is attained by a recombinant thermostable enzyme having the following physicochemical properties:

### (1) Action

Forming non-reducing saccharides having a trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of at least 3;



## 3

## (2) Molecular weight

About 69,000–79,000 daltons on sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE);

## (3) Isoelectric point (pI)

About 5.4–6.4 on isoelectrophoresis; and

## (4) Thermal stability

Substantially not inactivated even when incubated in an aqueous solution (pH 7.0) at 85° C. for 60 min.

The second object of the present invention is attained by a DNA which encodes the recombinant thermostable enzyme.

The third object of the present invention is attained by a replicable recombinant DNA which contains a self-replicable vector and the recombinant thermostable enzyme.

The fourth object of the present invention is attained by a transformant which is prepared by introducing the replicable recombinant DNA into an appropriate host.

The fifth object of the present invention is attained by a process for preparing the recombinant thermostable enzyme which comprises culturing the transformant in a nutrient culture medium, and collecting the formed recombinant thermostable enzyme from the culture.

The sixth object of the present invention is attained by a method for enzymatically converting reducing amylaceous saccharides which contains a step of allowing the recombinant thermostable enzyme to act on reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 to form non-reducing saccharides having a trehalose structure as an end unit.

#### BRIEF DESCRIPTION OF THE ACCOMPANYING DRAWINGS

FIG. 1 is a figure of the optimum temperature of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG. 2 is a figure of the optimum pH of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG. 3 is a figure of the thermostability of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG. 4 is a figure of the pH stability of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909).

FIG. 5 is a restriction map of the recombinant DNA pST35 according to the present invention.

FIG. 6 is a restriction map of the recombinant DNA pST36 according to the present invention.

#### DETAILED DESCRIPTION OF THE INVENTION

The recombinant thermostable enzyme according to the present invention forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 without inactivation even when allowed to react at a temperature exceeding 55° C.

The DNA according to the present invention expresses the production of the present enzyme by introducing the DNA into an appropriate self-replicable vector to form a replicable recombinant DNA, and introducing the replicable recombinant DNA into an appropriate host which does not produce the present enzyme in itself but readily proliferates.

The recombinant DNA according to the present invention expresses the production of the present enzyme by intro-

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ducing it into an appropriate host which does not produce the present enzyme but readily proliferates.

The transformant according to the present invention produces the present enzyme when cultured.

Culturing of the transformant by the present process facilitates the production of the present enzyme in a desired amount.

The present conversion method readily converts reducing amylaceous saccharide having a degree of glucose polymerization of at least 3 into non-reducing saccharides having a trehalose structure as an end unit.

The present invention has been accomplished based on the finding of a novel enzyme which forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3. Such an enzyme is obtainable from cultures of microorganisms of the species *Sulfolobus acidocaldarius* (ATCC 33909). The present inventors isolated such an enzyme by using in combination a various purification methods comprising column chromatography as a main technique, studied their properties and features, and revealed that the reality is a polypeptide with the following physicochemical properties:

## (1) Action

Forming non-reducing saccharides having a trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of at least 3;

## (2) Molecular weight

About 69,000–79,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);

## (3) Isoelectric point (pI)

About 5.4–6.4 on isoelectrophoresis; and

## (4) Optimum temperature

Exhibiting an optimum temperature of about 75° C. when incubated at a pH 5.5 for 60 min;

## (5) Optimum pH

Exhibiting an optimum pH of about 5.0–5.5 when incubated at 60° C. for 60 min;

## (6) Thermostability

Stable up to a temperature of about 85° C. even when incubated at a pH 7.0 for 60 min; and

## (7) pH Stability

Stable up to a pH of about 4.0–9.5 when incubated at 4° C. for 24 hours.

The followings are experiments which were conducted to reveal the physicochemical properties of a thermostable enzyme produced from *Sulfolobus acidocaldarius* (ATCC 33909):

#### EXPERIMENT 1

##### Preparation of Purified Enzyme

Into 500-ml flasks were put 100 ml aliquots of a liquid culture medium containing 0.1 w/v % polypeptone, 0.1 w/v % yeast extract, 0.2 w/v % ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water, and the flasks were sterilized by autoclaving at 120° C. for 20 min. After cooling the flasks a seed culture of *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated into each liquid culture medium in each flask, followed by the incubation at 75° C. for 24 hours under a rotary shaking condition of 130 rpm to obtain a first seed culture. About 5

## 5

L of a fresh preparation of the same liquid culture medium was put in a 10-L fermenter, sterilized similarly as above, cooled to 75° C., and adjusted to a pH 3.0, followed by inoculating one v/v % of the first seed culture into the sterilized liquid culture medium in the fermenter, and culturing the microorganisms at 75° C. for 24 hours under an aeration condition of 500 ml/min. Thereafter, about 250 L of a fresh preparation of the same liquid culture medium was placed in a 300-L fermenter, sterilized similarly as above, cooled to 75° C., and adjusted to a pH 3.0, followed by inoculating one v/v % of the second seed culture into the sterilized liquid culture medium, and culturing the microorganisms at 75° C. for 42 hours under an aeration condition of 100 L/min.

About 170 L of the resultant culture was filtered with an SF membrane, and the filtrate was centrifuged to obtain wet cells. About 258 g of the wet cells was suspended in 300 ml of 10 mM phosphate buffer (pH 7.0) and ultrasonicated to disrupt them. The cell debris thus obtained was centrifuged at 10,000 rpm for 30 min, and about 300 ml of the resultant supernatant was mixed with ammonium sulfate to give a saturation degree of 70 w/v %, allowed to stand at 4° C. for 24 hours, and centrifuged at 10,000 rpm for 30 min. The precipitate was collected, dissolved in an adequate amount of 10 mM Tris-HCl buffer (pH 8.5), and dialyzed against a fresh preparation of the same buffer for 24 hours. Thereafter, the dialyzed solution was centrifuged at 10,000 rpm for 30 min to obtain an about 600 ml of a supernatant with an enzymatic activity.

The supernatant was equally divided into 2 portions which were then respectively fed to a column packed with about 350 ml of "DEAE-TOYOPEARL", a gel for ion-exchange column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and fed with a linear gradient buffer ranging from 0 M to 0.3 M in 10 mM Tris-HCl buffer (pH 8.5). Fractions with an enzymatic activity, eluted at a concentration of about 0.1 M sodium chloride, were collected, pooled, and dialyzed for 10 hours against 10 mM Tris-HCl buffer (pH 8.5) containing one M ammonium sulfate. The dialyzed solution was centrifuged at 10,000 rpm for 30 min to remove insoluble substances, fed to a column packed with about 350 ml of "BUTYL-TOYOPEARL 650", a gel for hydrophobic chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5) containing one M ammonium sulfate, and fed with a linear gradient buffer ranging from 1 M to 0 M ammonium sulfate in 10 mM Tris-HCl buffer (pH 8.5).

Fractions with an enzymatic activity eluted at about 0.8 M ammonium sulfate were collected, pooled, dialyzed for 16 hours against 10 mM Tris-HCl buffer (pH 8.5) containing 0.2 M sodium chloride, and centrifuged to remove insoluble substances. The resultant supernatant was fed to a column packed with about 350 ml of "ULTROGEL® AcA", a gel for gel chromatography commercialized by Sepracor, Massachusetts, USA, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5) containing 0.2 M sodium chloride. Fractions with an enzymatic activity were collected from the eluate, pooled, and dialyzed against 10 mM Tris-HCl buffer (pH 8.5) for 16 hours. The dialyzed solution was centrifuged at 10,000 rpm for 30 min to remove insoluble substances, and the supernatant was fed to a column packed with about 10 ml of "MONO Q", a gel for ion-exchange chromatography commercialized by Pharmacia LKB Uppsala, Sweden, which had been previously equilibrated with 10 mM Tris-HCl buffer (pH 8.5), and eluted with a linear gradient buffer ranging from 0 M to 0.2

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M sodium chloride in 10 mM Tris-HCl buffer. Fractions with an enzymatic activity eluted at about 0.1 M sodium chloride were collected and pooled for use in the following experiments. The purified enzyme thus obtained had a specific activity of about 81 units/mg protein, and the yield was about 0.24 units per one L of the culture.

When the purified enzyme was in usual manner electrophoresed in 7.5 w/v % polyacrylamide gel, a substantially single band with an enzymatic activity was observed on the gel and revealing that it is extremely high in purity.

Throughout the specification the enzyme activity is expressed by the value measured on the following assay: Place 4 ml of 20 mM acetate buffer (pH 5.5) containing 1.25 w/v % maltopentaose in a test tube, add one ml of an adequately diluted enzyme solution to the test tube, and incubate the mixture solution at 60° C. for 60 min to effect enzymatic reaction. Thereafter, heat the reaction mixture at 100° C. for 30 min to suspend the enzymatic reaction. One ml of the reaction mixture thus obtained is diluted with deionized water by 10 times, and assayed for reducing power on the Somogyi-Nelson's method. As a control, a system using an enzyme solution, which has been heated at 100° C. for 30 min to inactivate the enzyme, is provided and similarly treated as above. One unit activity of the enzyme is defined as the amount of enzyme which reduces the reducing power of one  $\mu$ mol maltopentaose per min under the same conditions as mentioned above.

## EXPERIMENT 2

## Physicochemical Property of Thermostable Enzyme

## Experiment 2-1

## Action

An aqueous solution containing 10 w/v D of glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose or maltoheptaose as a substrate was prepared and mixed with 2 units/g substrate, d.s.b., of the purified enzyme in Experiment 1, and the mixture was enzymatically reacted at 60° C. and pH 5.5 for 48 hours. The reaction mixture was desalted in usual manner, and the saccharide composition of the resultant solution was analyzed on high-performance liquid chromatography (HPLC) using a column of "WAKO-BEADS WB-T-330", a column for HPLC commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan. The HPLC procedure was carried out under ambient temperature, and water was used as an eluant and fed to the column at a flow rate of 0.5 ml/min while monitoring the eluate on "MODEL RI-8012", a differential refractometer commercialized by Tosoh Corporation, Tokyo, Japan. The results were in Table 1.

TABLE 1

Substrate	Saccharide in reaction mixture	Composition (%)
Glucose	Glucose	100.0
Maltose	Maltose	100.0
Maltotriose	Glucose	9.2
	Maltose	18.4
Maltotetraose	Maltotriose	42.2
	$\alpha$ -glucosyltrehalose	30.2
	Glucose	6.7
	Maltose	2.7
	Maltotriose	9.0
	Maltotetraose	16.2
	$\alpha$ -glucosyltrehalose	8.2
	$\alpha$ -maltosyltrehalose	57.2

TABLE 1-continued

Substrate	Saccharide in reaction mixture	Composition (%)
Maltopentaose	Glucose	0.7
	Maltotetraose	2.0
	Maltopentaose	22.9
	$\alpha$ -maltosyltrehalose	0.9
	$\alpha$ -maltotriosyltrehalose	73.5
Maltohexaose	Glucose	0.9
	Maltopentaose	2.2
	Maltohexaose	23.1
	$\alpha$ -maltotriosyltrehalose	5.6
	$\alpha$ -maltotetraosyltrehalose	68.2
Maltoheptaose	Glucose	1.0
	Maltohexaose	1.4
	Maltoheptaose	23.4
	$\alpha$ -Maltotetraosyltrehalose	4.2
	$\alpha$ -Maltopentaosyltrehalose	70.0

The results in Table 1 show that the purified enzyme acted on reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose to form non-reducing saccharides having a trehalose structure as an end unit such as  $\alpha$ -glucosyltrehalose,  $\alpha$ -maltosyltrehalose,  $\alpha$ -maltotriosyltrehalose,  $\alpha$ -maltotetraosyltrehalose and  $\alpha$ -maltopentaosyltrehalose. In addition to these non-reducing saccharides and intact substrates, glucose and low molecular weight maltooligosaccharides as estimable hydrolysates of the substrates, were detected in the reaction mixtures, and this indicates that the purified enzyme has a hydrolytic activity. The yields of the non-reducing saccharides and hydrolysates from the substrates were respectively 30.2% and 27.6% for maltotriose, 65.4% and 18.4% for maltotetraose, and about 74–75% and about 2–3% for maltopentaose, maltohexaose and maltoheptaose. The purified enzyme formed non-reducing saccharides from maltooligosaccharides having a degree of glucose polymerization of at least 5 in a satisfactory yield, and less hydrolyzed the substrates, but did not newly form any saccharide from glucose and maltose.

#### Experiment 2-2

##### Molecular weight

In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680–685 (1970), the purified enzyme in Experiment 1 was electrophoresed on SDS-PAGE to give a single protein band with an enzymatic activity at a position corresponding to about 69,000–79,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons),  $\beta$ -galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and ovalbumin (MW=45,000 daltons).

#### Experiment 2-3

##### Isoelectric Point

The purified enzyme in Experiment 1 gave an isoelectric point of about 5.4–6.4 on isoelectrophoresis using a polyacrylamide gel containing 2 w/v % ampholine.

#### Experiment 2-4

##### Optimum temperature

As is shown in FIG. 1, the optimum temperature of the purified enzyme in Experiment 1 was about 75° C. when incubated in usual manner in 20 mM acetate buffer (pH 5.5) at different temperatures for 60 min.

#### Experiment 2-5

##### Optimum pH

As is shown in FIG. 2, the optimum pH of the purified enzyme in Experiment 1 was about 5.0–5.5 when incubated

in usual manner at 60° C. for 60 min in McIlvaine buffer with different pHs.

#### Experiment 2-6

##### Thermal stability

As is shown in FIG. 3, the purified enzyme in Experiment 1 was stable up to a temperature of about 85° C. when incubated in usual manner in 10 mM phosphate buffer (pH 7.0) for 60 min.

#### Experiment 2-7

##### pH Stability

As is shown in FIG. 4, the purified enzyme in Experiment 1 was stable at a pH in the range of about 4.5–9.5 when incubated in usual manner at 25° C. for 16 hours in McIlvaine buffer or 50 mM sodium carbonate/sodium hydrogen carbonate buffer with different pHs.

#### Experiment 2-8

##### Amino acid sequence containing the N-terminal

The amino acid sequence containing the N-terminal of the purified enzyme in Experiment 1 was analyzed on "MODEL 473 A", a gas-phase protein sequencer commercialized by Perkin-Elmer Corp., Instrument Div., Norwalk, USA, and revealed that it has the amino acid sequence in SEQ ID NO:3.

#### Experiment 2-9

##### Partial amino acid sequence

An adequate amount of the purified enzyme in Experiment 1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4° C. for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed in a container, admixed with 10  $\mu$ g lysyl endopeptidase, and incubated at 30° C. for 48 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "μBONDAPAK C18", a column for HPLC commercialized by Japan Millipore Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 16 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of aqueous acetonitrile from 16 to 48 v/v %, and collecting fractions containing a peptide fragment eluted about 11 min after the initiation of the feeding. The fractions were pooled, dried in vacuo, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragment was analyzed and revealed to have an amino acid sequence in SEQ ID NO:4.

Such an enzyme having these physicochemical properties has not been known, and meaning that it is a novel enzyme.

A chromosomal DNA of *Sulfolobus acidocaldarius* (ATCC 33909) was screened by using an oligonucleotide as a probe which had been chemically synthesized based on the partial amino acid sequences in SEQ ID NOs:3 and 4, and this yielded a DNA fragment having a base sequence from the 5'-terminus consisting of about 2,200 base pairs in SEQ ID NO:2. The base sequence of the thermostable enzyme was decoded and revealing that it consists of 720 amino acids and has a partial amino acid sequence from the N-terminal in SEQ ID NO:1.

The sequential experimental steps used to reveal the amino acid sequence and the base sequence in SEQ ID NOs:1 to 2 are summarized in the below:

- (1) The thermostable enzyme was isolated from a culture of a donor microorganism, highly purified, and determined for the N-terminal amino acid sequence. The purified enzyme was partially hydrolyzed with protease, and from which a peptide fragment was isolated and determined for amino acid sequence;

- (2) A chromosomal DNA was isolated from a donor microorganism, purified and partially digested with a restriction enzyme to obtain a DNA fragment consisting of about 2,000–6,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cleaved with a restriction enzyme, to obtain a recombinant DNA;
- (3) The recombinant DNA thus obtained was introduced into *Escherichia coli* to obtain transformants, and from which an objective transformant containing a DNA which encodes the objective enzyme was selected by the colony hybridization method using as a probe an oligonucleotide which had been chemically synthesized based on the above partial amino acid sequence; and
- (4) The recombinant DNA was obtained from the transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence, that could be estimated from the base sequence, with the aforesaid amino acid sequence confirmed that the base sequence encodes the enzyme.

The following Experiments 3 and 4 will concretely explain the above steps (2) to (4), and the techniques in themselves used therein are well known in this art, for example, those described by J. Sumbruck et al. in "*Molecular Cloning A Laboratory Manual*", 2nd edition, published by Cold Spring Harbor Laboratory Press, USA (1989).

### EXPERIMENT 3

#### Preparation of Recombinant DNA Containing DNA which Encodes Thermostable Enzyme, and Transformant Obtained Therewith

##### Experiment 3-1

##### Preparation of chromosomal DNA

To 500-ml flasks were placed about 100 ml aliquots of a liquid culture medium consisting of 0.1 w/v % polypeptone, 0.1 w/v % yeast extract, 0.2 w/v % ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water, and the flasks were sterilized by autoclaving at 120° C. for 20 min, cooled, and adjusted to a pH 3.0 by the addition of sulfate. A seed culture of *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated into each flask, incubated at 75° C. for 24 hours under a rotary shaking condition of 130 rpm to obtain a seed culture. About 5 L of a fresh preparation of the same liquid nutrient culture medium was placed in a 10-L fermenter, sterilized similarly as above, cooled to 75° C., adjusted to a pH 3.0, and inoculated with one v/v % of the seed culture, followed by the incubation at 75° C. for 24 hours under an aeration condition of 500 ml/min.

The resultant cells were collected by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37° C. for 30 min. The resultant was freeze-dried at –80° C. for one hour, admixed with TES buffer (pH 9.0), heated to 60° C., and admixed with a mixture solution of TES buffer and phenol, and the resultant mixture was chilled with ice and centrifuged to obtain a supernatant. To the supernatant was added 2 fold volumes of cold ethanol to precipitate a crude chromosomal DNA which was then collected, dissolved in SSC buffer (pH 7.1), admixed with 7.5 µg ribonuclease and 125 µg protease, and

incubated at 37° C. for one hour. Thereafter, a mixture solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA. The resultant solution was admixed with cold ethanol, followed by collecting the formed sediment containing the chromosomal DNA. The purified chromosomal DNA thus obtained was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the solution was freeze-dried at –80° C.

##### Experiment 3-2

##### Preparation of recombinant DNA pST35 and transformant ST35

One ml of the purified chromosomal DNA in Experiment 3-1 was placed in a container, admixed with about 35 units of Sau 3AI, a restriction enzyme, and enzymatically reacted at 37° C. for 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 2,000–6,000 base pairs by sucrose density-gradient ultracentrifugation. One µg of Bluescript II SK(+), a plasmid vector, was weighed, subjected to the action of Bam HI, a restriction enzyme, to completely digest the plasmid vector, and admixed with 10 µg of the DNA fragment and 2 units of T4 DNA ligase. The mixture was allowed to stand at 4° C. overnight to ligate the DNA fragment to the plasmid vector. To the resultant recombinant DNA was added 30 µl of "Epicurian Coli® XLI-Blue", a competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilling conditions for 30 min, heated to 42° C., admixed with SOC broth, and incubated at 37° C. for one hour to introduce the recombinant DNA into *Escherichia coli*.

The transformant thus obtained was inoculated into agar plate (pH 7.0) containing 50 µg/ml of 5-bromo-4-chloro-3-indolyl-β-galactoside, and cultured at 37° C. for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 5,000 colonies formed on the agar plate. Based on the amino acid sequence Asn-Leu-Trp-Tyr-Phe-Lys-Asp (amino acids 22–28 of SEQ ID NO:3), probe 1 represented by the base sequence of 5'-AAYYTNTGGTAYTTTAAARGA-3' (SEQ ID NO:7) was chemically synthesized, labelled with <sup>32</sup>P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 15 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 15 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503–517 (1975), hybridized with probe 2 having the base sequence of 5'-GARGARTGGCAYWSNATHAT-3' (SEQ ID NO:8) which had been chemically synthesized based on the amino acid sequence of Glu-Glu-Trp-His-Ser-Ile-Ile amino acids 2–8 of SEQ ID NO:4—and labelled with <sup>32</sup>P, followed by selecting a recombinant DNA which exhibited a strong hybridization. The recombinant DNA and transformant were respectively named "pST35" and "ST35".

The transformant ST35 was inoculated into L-broth (pH 7.0) containing 100 µg/ml ampicillin, and cultured at 37° C. for 24 hours with a rotary shaker. After completion of the culture, the cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract the recombinant DNA. The resultant extract was in usual manner purified and analyzed to find that the recombinant DNA pST35 consists of about 6,200 base pairs and has a DNA, which encodes the enzyme and consists of about 2,200 base pairs, in the downstream of the cleave site of Eco RV, a restriction enzyme.



## Experiment 3-3

Production of recombinant thermostable enzyme by transformant ST35

To 500-ml flasks were added about 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of 0.1 w/v % polypeptone, 0.1 w/v % yeast extract, 0.2 w/v % ammonium sulfate, 0.05 w/v % potassium dihydrogen phosphate, 0.02 w/v % magnesium sulfate heptahydrate, 0.02 w/v % potassium chloride, and water. The flasks were sterilized by autoclaving at 120° C. for 20 min, cooled, admixed with 50 µg/ml ampicillin, and inoculated with a seed culture of transformant ST35 in Experiment 3-2, followed by culturing the transformant at 37° C. for 24 hours under a rotary shaking condition of 130 rpm to obtain a seed culture. About 5 L of a fresh preparation of the same liquid culture medium was placed in a 10-L fermenter, sterilized similarly as above, cooled to 37° C., admixed with 50 µg/ml ampicillin, inoculated with one v/v % of the seed culture, followed by the incubation at 37° C. for 24 hours under an aeration condition of 500 ml/min.

The resultant culture was in usual manner treated with ultrasonic to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was admixed with ammonium sulfate to give a saturation degree of 70 w/v %, allowed to stand at 4° C. for 24 hours, and centrifuged to obtain a precipitate which was then dissolved in a small amount of 10 mM phosphate buffer (pH 8.5). The resultant solution was dialyzed against a fresh preparation of the same buffer for 10 hours, and the dialyzed solution was assayed for enzymatic activity and revealing that one L of the culture yielded about 8.0 units of the recombinant thermostable enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue strain or *Sulfolobus acidocaldarius* (ATCC 33909) was inoculated into a fresh preparation of the same liquid culture medium but free of ampicillin. In the case of culturing *Sulfolobus acidocaldarius* (ATCC 33909), it was cultured and treated similarly as above except that the initial pH of the nutrient culture medium and the culturing temperature were respectively set to 3.0 and 75° C. Assaying the resultant enzymatic activity, one L culture of *Sulfolobus acidocaldarius* (ATCC 33909) yielded about 1.8 units of the thermostable enzyme, and the yield was significantly lower than that of transformant ST35. *Escherichia coli* XLI-Blue strain used as a host did not form the thermostable enzyme.

Thereafter, the recombinant thermostable enzyme produced by the transformant ST35 was purified similarly as in Experiments 1 and 2 and examined for properties and features and revealing that it has substantially the same physicochemical properties of the thermostable enzyme from *Sulfolobus acidocaldarius* (ATCC 33909) because (i) the recombinant thermostable enzyme has a molecular weight of about 69,000–79,000 daltons on SDS-PAGE and an isoelectric point of about 5.4–6.4 on isoelectrophoresis, and (ii) it is not substantially inactivated even when incubated in an aqueous solution (pH 7.0) at 85° C. for 60 min. These results indicate that the present thermostable enzyme can be prepared by the recombinant DNA technology with a significantly improved yield.

## EXPERIMENT 4

Preparation of Complementary DNA, and  
Determination of Base Sequence and Amino Acid  
Sequence

Two µg of the recombinant DNA pST35 in Experiment 3-2 was weighed, degenerated by the addition of 2 M

aqueous sodium hydroxide solution, and admixed with an adequate amount of cold ethanol, followed by collecting the resultant sediment containing a template DNA and drying the sediment in vacuo. To the template DNA were added 50 pmole/ml of a chemically synthesized primer having the base sequence of 5'-GTAAAACGACGGCCAGT-3' SEQ ID NO:19 and 10 µl of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and sodium chloride, and the mixture was incubated at 65° C. for 2 min to effect annealing. The resultant mixture was admixed with 2 µl of an aqueous solution containing 7.5 µM dATP, dGTP and dTTP respectively, 0.5 µl of [ $\alpha$ -<sup>32</sup>P]dCTP (2 mCi/ml), one µl of 0.1 M dithiothreitol, and 2 µl of 1.5 units/ml T7 DNA polymerase, followed by the incubation at 25° C. for 5 min to extend the primer from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was obtained.

The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5 µl of 50 mM aqueous sodium chloride solution containing 80 µM dNTP and 8 µM ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37° C. for 5 min, followed by suspending the reaction by the addition of 4 µl of 98 v/v % aqueous, formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue and 0.05 w/v % xylene cyanol. The reaction mixture was placed in a container, heated in a boiling-water bath for 3 min, placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying it and subjecting the resultant to autoradiography.

Analyses of the DNA fragments separated on the radiogram revealed that the complementary chain DNA contains the base sequence consisting of 2,200 base pairs in SEQ ID NO:5. An amino acid sequence that could be estimated from the base sequence was in SEQ ID NO:5, and it was compared with the partial amino acid sequences in SEQ ID NOs:3 and 4, and revealing that the partial amino acid sequence in SEQ ID NO:3 corresponded to that positioning from 1 to 30 in SEQ ID NO:5, and that in SEQ ID NO:4 corresponded to that positioning from 468 to 478 in SEQ ID NO:5. These results indicate that the present recombinant thermostable enzyme has the amino acid sequence from the N-terminal in SEQ ID NO:1, and, in the case of the DNA derived from *Sulfolobus acidocaldarius* (ATCC 33909), the amino acid sequence is encoded by the base sequence from the 5'-terminus in SEQ ID NO:2.

As is explained in the above, the thermostable enzyme, which forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylose saccharides having a degree of glucose polymerization of at least 3, was found as a result of the present inventors' long-term research. The thermostable enzyme has distinct physicochemical properties from those of other conventional enzymes. The present invention is to produce the thermostable enzyme by using the recombinant DNA technology. The present recombinant thermostable enzyme, as well as its preparation and uses, will be explained in detail with reference to the later described Examples.

The recombinant thermostable enzyme as referred to in the present invention means thermostable enzymes in general which are preparable by the recombinant DNA technology and capable of forming non-reducing saccharides having a trehalose structure as an end unit from reducing amylose saccharides having a degree of glucose polymerization of at least 3. Generally, the recombinant thermo-

stable enzyme according to the present invention has a revealed amino acid sequence, and, as an example, the amino acid sequence from the N-terminal as shown in SEQ ID NO:1, and homologous ones to it can be mentioned. Variants having amino acid sequences homologous to the one in SEQ ID NO:1 can be obtained by replacing one or more bases in SEQ ID NO:1 with other bases without substantially alternating the inherent physicochemical properties. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, the ingredients and components of nutrient culture media for culturing transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have the inherent physicochemical properties but defect one or more amino acids in SEQ ID NO:1, or those which have one or more amino acids added newly to the N-terminal after the DNA expression as the result of the modification of intracellular enzymes of the hosts. Such variants can be used in the present invention as long as they have the desired physicochemical properties.

The recombinant thermostable enzyme can be obtained from cultures of transformants containing a specific DNA. Examples of such transformants usable in the present invention can be prepared by introducing into hosts a DNA which has either the base sequence from the 5'-terminus in SEQ ID NO:2 or a homologous base sequence to it or a complementary base sequence to them. These base sequences may be modified by replacing one or more bases of them without alternating the amino acid sequences encoded by them by means of the degeneracy of genetic code. Needless to say, one or more bases in such base sequences which encode the recombinant thermostable enzyme or their variants can be readily replaced with other bases to allow the DNA to express the objective thermostable enzyme production in hosts.

The DNA usable in the present invention includes those are derived from natural resources and those which are artificially synthesized as long as they have the aforesaid base sequences. The natural resources for the DNA according to the present invention are, for example, microorganisms of the genus *Sulfolobus* such as *Sulfolobus acidocaldarius* (ATCC 33909), and from which genes containing the present DNA can be obtained. The aforementioned microorganisms can be inoculated in nutrient culture media and cultured for about 1–3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or  $\beta$ -glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, when treated the cells with an ultrasonic disintegrator, they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or with freezing and thawing method. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment generally used in this field. To artificially synthesize the present DNA, it can be chemically synthesized by using the base sequence in SEQ ID NO:2, or can be obtained in a plasmid form by inserting a DNA, which encodes the amino acid sequence in SEQ ID NO:1, into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the objective DNA from the cells.

Such a DNA is generally introduced into hosts in a recombinant DNA form. Generally, the recombinant DNA contains the aforesaid DNA and a self-replicable vector, and it can be prepared with a relative easiness by the recombinant DNA technology in general when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pKK223-3, pUB110, pTZ4, pC194, pHV14, TRp7, TEp7, pBS7, etc.; and phage vectors such as  $\lambda$ gt- $\lambda$ C,  $\lambda$ gt- $\lambda$ B,  $\rho$ 11,  $\phi$ 1,  $\phi$ 105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+), pKK223-3,  $\lambda$ gt- $\lambda$ C and  $\lambda$ gt- $\lambda$ B are satisfactorily used when the present DNA should be expressed in *Escherichia coli*, while pUB110, pTZ4, pC194,  $\rho$ 11,  $\phi$ 1 and  $\phi$ 105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRp7, TEp7 and pBS7 are advantageously used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such vectors in the present invention may be conventional ones in generally used in this field. A gene containing the present DNA and a self-replicable vector are first digested with a restriction enzyme and/or ultrasonic, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly *Sau* 3AI, *Eco* RI, *Hind* III, *Bam* HI, *Sal* I, *Xba* I, *Sac* I, *Pst* I, *Ban* III, *Spe* I, etc., facilitate the ligation of the DNA fragments and vector fragments. To ligate the DNA fragments with the vector fragments, they are, if necessary, annealed and subjected to the action of a DNA ligase in vivo or in vitro. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts, and culturing the resultant transformants.

The recombinant DNA thus obtained can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomyces and yeasts. In the case of using *Escherichia coli* as a host, the DNA can be introduced thereinto by culturing the host in the presence of the recombinant DNA and calcium ion, while in the case of using a microorganism of the genus *Bacillus* as a host the competent cell method and the colony hybridization method can be used. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing reducing amylaceous saccharides having a degree of glucose polymerization of at least 3, and selecting the objective transformants which form non-reducing saccharides having a trehalose structure as an end unit from the reducing amylaceous saccharides.

The transformants thus obtained intra- and extracellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid culture media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with small amounts of amino acids and vitamins can be used in the invention. Examples of the carbon sources are saccharides such as unprocessed starch, starch hydrolysate, glucose, fructose, sucrose and trehalose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia and salts thereof, urea, nitrate, peptone, yeast extract, defatted soy bean, corn steep liquor, and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 20–65° C. and a pH of 2–9 for about 1–6 days under aerobic conditions by the aeration-agitation method.

Such cultures can be used intact as a crude enzyme, and, usually, cells in the cultures may be disrupted prior to use with ultrasonic and/or cell-wall lysis enzymes, followed by separating the thermostable enzyme from intact cells and cell debris by filtration and/or centrifugation and purifying the enzyme. The methods to purify the enzyme include conventional ones in general. From cultures intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, separatory sedimentation, gel filtration chromatography, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the recombinant thermostable enzyme according to the present invention has a specific feature of forming non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 even when allowed to act on at a temperature exceeding 55° C. The formed non-reducing saccharides have a satisfactorily mild and high-quality sweetness as well as an adequate viscosity and moisture-retaining ability, and, as a great advantageous feature, they can sweeten food products without fear of causing unsatisfactory coloration and deterioration because they have no reducing residue within their molecules. With these features a variety of amylaceous saccharides, which have been put aside because of their reducibilities, can be converted into saccharides which have a satisfactory handleability, usefulness, and no substantial reducibility or extremely-reduced reducibility.

Explaining now the conversion method in more detail, reducing starch hydrolysates, which are obtainable by partially hydrolyzing amylaceous saccharides such as starch, amylopectin and amylose with acids and/or amylases, can be usually used as the substrate for the present recombinant thermostable enzyme. Such reducing starch hydrolysate can be obtained by conventional methods generally used in this field, and examples of such include one or more maltooligosaccharides having a degree of glucose polymerization of at least 3, for example, maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose. As is described in "*Handbook of Amylases and Related Enzymes*", 1st edition (1988), edited by The Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England,  $\alpha$ -amylase, maltotetraose-forming amylase, maltopentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amylaceous saccharides used in the present invention, and, the use of any one of these amylases facilitates the production of mixtures of amylaceous saccharides rich in reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 in a considerably-high yield. If necessary, the combination use of the amylases and starch debranching enzymes such as pullulanase and isoamylase can increase the yield of the reducing amylaceous saccharides used as the substrate for the present recombinant thermostable enzyme.

In the enzymatic conversion method according to the present invention, the present recombinant thermostable enzyme is generally allowed to coexist in an aqueous solution containing one or more of the above reducing amylaceous saccharides as a substrate, followed by the enzymatic reaction at a prescribed temperature and pH until a desired amount of the objective reducing amylaceous saccharides is formed. Although the enzymatic reaction proceeds even below a concentration of 0.1 w/w %, d.s.b., of a substrate, a concentration of 2 w/w % or higher, d.s.b.,

preferably, in the range of 5–50 w/w %, d.s.b., of a substrate can be satisfactorily used when used the present conversion method in an industrial-scale production. The temperature and pH used in the enzymatic reaction are set to within the range of which does not inactivate the recombinant thermostable enzyme and allows the enzyme to effectively act on substrates, i.e. a temperature of higher than 55° C. but not higher than 85° C., preferably, a temperature in the range of about 56–70° C., and a pH of 4–7, preferably, a pH in the range of about 5–6. The amount and reaction time suitable for the present recombinant thermostable enzyme are chosen depending on the enzymatic reaction condition. Thus, the present recombinant thermostable enzyme converts reducing amylaceous saccharides having a degree of glucose polymerization of at least 3 into non-reducing saccharides having a trehalose structure as an end unit, e.g. the conversion rate reaches up to about 74% when acts on maltopentaose.

The reaction mixtures obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use: Insoluble substances are eliminated from the reaction mixtures by filtration and centrifugation, and the resultant solutions are decolorized with activated charcoals, desalted and purified on ion exchangers, and concentrated into syrupy products. Depending on their use, the syrupy products are dried in vacuo and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the aforesaid syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel for saccharide separation, separatory sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a relatively-large amount of reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange chromatography as disclosed in Japanese Patent Laid-Open Nos. 23,799/83 and 72,598/83, and such a method produces non-reducing saccharide-rich products on an industrial scale and in a considerably-high yield.

The non-reducing saccharides thus obtained have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners: For example, they can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. Since the non-reducing saccharides almost qualitatively form trehalose when received an enzymatic action of a trehalose-releasing enzyme as disclosed in Japanese Patent Application No. 79,291/94, they can be used as an intermediate for producing trehalose which could not have been readily prepared.

The following Examples explain in detail the preparation of the present recombinant thermostable enzyme, and the enzymatic conversion method of reducing amylaceous saccharides using the enzyme:

#### EXAMPLE A-1

##### Preparation of Recombinant Thermostable Enzyme

In 500-ml flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of one w/v % polypeptone, 0.5 w/v % yeast extract, 0.5 w/v % sodium chloride, and water, and to each flask was sterilized by autoclaving at 120° C. for 20 min, and admixed with 50  $\mu$ g/ml ampicillin. Thereafter, the flasks were cooled and

inoculated with the transformant ST35 obtained by the method in Experiment 3-2, followed by the culture of the transformant at 37° C. for 24 hours under a rotary shaking condition of 130 rpm to obtain a seed culture. To 30-L fermenter was placed about 18 L of a fresh preparation of the same liquid culture medium, sterilized similarly as above, cooled to 37° C., admixed with 50 µg/ml ampicillin, and inoculated with one v/v % of the seed culture, followed by the culture at 37° C. for 24 hours under aeration and agitation conditions.

The resultant culture was treated with ultrasonic to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances, followed by assaying the enzymatic activity in the supernatant to find that one L of the culture contained about 75 units of the present recombinant thermostable enzyme. The culture supernatant was purified by the method in Experiment 1 to obtain an about 10 ml aqueous solution containing about 57 units/ml of the present recombinant thermostable enzyme having a specific activity of about 80 units/mg protein.

#### EXAMPLE A-2

##### Preparation of Recombinant Thermostable Enzyme

##### Example A-2 (a)

##### Preparation of transformant

Ten oligonucleotides, which were chemically synthesized by conventional method and had the following base sequences represented by 5'-GATCCGTTCTGGCAAATATTCTGAAATGAGCTGT-3' (SEQ ID NO:9), 5'-TGACAATTAATCATCGGCTCGTCTAATGTGTGGAATTCTGATTCGA-3' (SEQ ID NO:10), 5'-ATTTTAAATAAAAATCAGGAGGAAAAAATATGATATCAGCAACCTACA-3' (SEQ ID NO:11), 5'-GATTACAGTTAAATAAGAATTTTAATTTTGGTGACGTAATCGATGAA-3' (SEQ ID NO:12), 5'-TTCAGTAGTTAGAAATGTGATGAAGGCCTGCGGCCTGCGAGAGCTCA-3' (SEQ ID NO:13), 5'-CGATGATTAATTGTCAACAGCTCATTTTCAAGAATTTTGCCAGAAGC-3' (SEQ ID NO:14), 5'-TTTTATTAAAAAATTCGAATCAGAATTCCACACATTAGACGAGC-3' (SEQ ID NO:15), 5'-TTAACTGTAATCTGTAGGTTGCTGATATCATATTTTTCCTCCTGA-3' (SEQ ID NO:16), 5'-TAGTGAATTCTACGATTACGTCACCAAAATTAATAATTCTTAT-3' (SEQ ID NO:17), and 5'-AGCTTGAGCTCTGCAGCGGCCGCAGGCCTTCATCACATTCTAAC-3' (SEQ ID NO:18), were mixed in an appropriate ratio, and the mixture was successively incubated at 100° C., 65° C., 37° C. and 20° C. for each 20 min to anneal them. The resultant double strand DNA having the base sequence in SEQ ID NO:6 was admixed with "pKK223-3", a plasmid vector commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, which had been cleaved with restriction enzymes Bam HI and Hind III, and the mixture was allowed to stand at 4° C. overnight in the presence of T4 DNA ligase to effect ligation and resulting in the formation of a first recombinant DNA having the base sequences of bases 1 through 59 and those 2,149 through 2,160 of SEQ ID NO:2. The first recombinant DNA corresponded to the base sequence in SEQ ID NO:2 wherein the first amino acid "G (guanine)" was replaced with "A (adenine)".

A recombinant DNA pST35 obtained by the method in Experiment 3-2 was cleaved with recombinant enzymes Ban III and Spe I to obtain a DNA fragment consisting of about

2,090 base pairs having a base sequence of bases 60 through 2,148 of SEQ ID NO:2. Similarly as in the above, the DNA fragment was ligated to the first recombinant DNA which had been cleaved with restriction enzymes Ban III and Spe I to obtain the present recombinant DNA pST36 having 2,160 base pairs corresponding to the base sequence of SEQ ID NO:2 wherein the first base "G (guanine)" was replaced with "A (adenine)" without alternating the amino acid sequence of SEQ ID NO:1.

In accordance with the method in Experiment 3-2, the recombinant DNA pST36 was introduced into "BMH71-18", a competent cell commercialized by Takara Shuzo Co., Ltd., Tokyo, Japan, to obtain transformant ST36 having a DNA encoding the present recombinant thermostable enzyme. The transformant ST36 was cultured by the method in Experiment 3-2, and the proliferated cells were collected from the resultant culture. A recombinant DNA was eluted from the cells and analyzed and revealing that it consists of about 6,700 base pairs, and, as shown in FIG. 6, it has a DNA located in the downstream of the cleavage site of Eco RV, a restriction enzyme.

##### Example A-2 (b)

Preparation of recombinant thermostable enzyme from transformant

The transformant ST36 was cultured similarly as in Example A-1 except that a liquid nutrient culture medium (pH 7.0) consisting of 2 w/v % maltose, 4 w/v % "N-Z-SOY PEPTONE commercialized by Sigma Chemicals Co., St. Louis, Mo., USA, 2 w/v % yeast extract, 0.5 w/v % sodium dihydrogen phosphate, 200 µg/ml ampicillin, and water was used. The resultant culture was treated with ultrasonic to disrupt cells, and the cell suspension was centrifuged to remove insoluble substances, followed by assaying the recombinant thermostable enzyme activity in the resultant supernatant and revealing that one L culture yielded about 120,000 units of the objective recombinant thermostable enzyme. The supernatant was purified by the method in Experiment 1 to obtain an about 4,040 ml aqueous solution containing about 230 units/ml of the recombinant thermostable enzyme with a specific activity of about 80 units/mg protein.

The purified enzyme was assayed for properties and features by the method in Experiment 2 and revealing that it had a molecular weight of about 69,000–79,000 daltons on SDS-PAGE and a pI of about 5.4–6.4 on isoelectrophoresis, and was not substantially inactivated even when incubated in an aqueous solution (pH 7.0) at 85° C. for 60 min. These physicochemical properties were substantially the same as those of the enzyme from a donor microorganism of *Sulfolobus acidocaldarius* (ATCC 33909).

#### EXAMPLE B-1

##### Conversion into Syrupy Product Containing Non-Reducing Saccharide

Six w/w %, d.s.b., of a potato starch suspension was gelatinized by heating, adjusted to pH 4.5 and 50° C., admixed with 2,500 units/g starch, d.s.b., of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted for 20 hours. The reaction mixture was adjusted to pH 6.5, autoclaved at 120° C. for 10 min to inactivate the remaining enzyme, rapidly cooled to 40° C., admixed with 150 units/g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted for 20 hours. The reaction mixture was autoclaved at



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120° C. for 20 min to inactivate the remaining enzyme, cooled to 60° C., adjusted to pH 5.5, admixed with one unit/g starch, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example A-1, and enzymatically reacted for 96 hours. The resultant reaction mixture was heated at 97° C. for 30 min to inactivate the remaining enzyme, cooled and filtered, and the resultant filtrate was in usual manner decolored with an activated charcoal, desalted and purified with an ion exchanger and concentrated to obtain an about 70 w/w % syrup, d.s.b., in a yield of about 90% to the material starch, d.s.b.

The syrup had a low DE (dextrose equivalent) of 24.5 and contained 12.1 w/w %  $\alpha$ -glucosyltrehalose, 5.4 w/w %  $\alpha$ -maltosyltrehalose, 30.0 w/w %  $\alpha$ -maltotriosyltrehalose, 1.4 w/w %  $\alpha$ -maltotetraosyltrehalose and 2.0 w/w %  $\alpha$ -maltopentaosyltrehalose. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in composition in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

## EXAMPLE B-2

## Conversion into Powdery Product Containing Non-Reducing Saccharide

A syrupy product containing non-reducing saccharides obtained by the method in Example B-1 was column chromatographed using a strong-acid cation exchange resin to increase the content of the non-reducing saccharides. The procedures were as follows: Four jacketed-stainless steel columns, 5.4 cm in diameter and 5 m in length each, were packed to homogeneity with "XT-1016 (Na<sup>+</sup>-form, polymerization degree of 4%)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series to give a total column length of 20 m. The columns were fed with a syrupy product, adequately diluted with water, in a volume of about 5 v/v % to the resin and at an inner column temperature of 55° C., and fed with 55° C. hot water at an SV (space velocity) 0.13 to elute saccharide components. Fractions rich in non-reducing saccharides were collected, pooled, concentrated, dried in vacuo and pulverized to obtain a powdery product rich in non-reducing saccharides in a yield of about 64% to the material, d.s.b.

The product had a low DE of 4.8 and contained 12.8 w/w %  $\alpha$ -glucosyltrehalose, 11.5 w/w %  $\alpha$ -maltosyltrehalose, 46.6 w/w %  $\alpha$ -maltotriosyltrehalose, 2.3 w/w %  $\alpha$ -maltotetraosyltrehalose and 3.4 w/w %  $\alpha$ -maltopentaosyltrehalose, d.s.b. Similarly as the product in Example B-1, the product has a mild and moderate sweetness and an adequate viscosity and moisture-retaining ability, and can be satisfactorily used in compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

## EXAMPLE B-3

## Conversion into Syrupy Product Containing Non-Reducing Saccharide

To 33 w/w %, d.s.b., of corn starch suspension was added calcium carbonate to give a final concentration of 0.1 w/w %, d.s.b., adjusted to pH 6.5, and admixed with 0.2 units/g starch, d.s.b., of "TERMAMYL 60L", an  $\alpha$ -amylase speci-

## 20

men commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95° C. for 15 min to liquefy the starch. The mixture was autoclaved at 120° C. for 10 min to inactivate the remaining enzyme, cooled to 55° C., admixed with 5 units/g starch, d.s.b., of a maltotetraose-forming enzyme commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted for 6 hours. The reaction mixture was mixed with 30 units/g starch, d.s.b., of " $\alpha$ -amylase 2A", an  $\alpha$ -amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, enzymatically reacted at 65° C. for 4 hours, autoclaved at 120° C. for 10 min to inactivate the remaining enzyme, cooled to 65° C., adjusted to pH 5.5, admixed with 2 units/g starch, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example A-1, and enzymatically reacted for 48 hours. The reaction mixture thus obtained was heated at 97° C. for 30 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with ion exchangers, and concentrated to obtain an about 70 w/w % syrupy product in a yield of about 90% to the material starch, d.s.b.

The product had a low DE of 17.1 and contained 8.9 w/w %  $\alpha$ -glucosyltrehalose, 29.3 w/w %  $\alpha$ -maltosyltrehalose, 0.8 w/w %  $\alpha$ -maltotriosyltrehalose, 0.7 w/w %  $\alpha$ -maltotetraosyltrehalose and 0.7 w/w %  $\alpha$ -maltopentaosyltrehalose, d.s.b. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

## EXAMPLE B-4

## Conversion into Powdery Product Containing Non-Reducing Saccharide

To a 20 w/w % aqueous solution containing a high-purity maltopentaose commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was added 1.0 unit/g maltopentaose, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example A-1 to effect an enzymatic reaction at 70° C. for 48 hours. A reaction mixture, wherein about 72% of the maltopentaose had been converted into  $\alpha$ -maltotriosyltrehalose, was heated at 97° C. for 30 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner, desalted and purified with an ion exchanger, and concentrated.

The concentrate was subjected to the same column chromatographic fractionation in Example B-1, and  $\alpha$ -maltotriosyl rich fractions were collected, pooled, and, in usual manner, purified, concentrated and spray dried to obtain a powdery product rich in non-reducing saccharides in a yield of about 26 w/w % to the material, d.s.b.

The product, having an extremely low DE of less than 0.2 and an  $\alpha$ -maltotriosyltrehalose content of 99.0 w/w %, d.s.b., is relatively low in sweetness, and it can be satisfactorily used in compositions in general such as food products, cosmetics and pharmaceuticals as a taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

## EXAMPLE B-5

## Conversion into Powdery Product Containing Crystalline Trehalose

Forty parts by weight of "PINE-DEX #4", a reducing amylaceous saccharide produced by Matsutani Chemical

Ind., Co., Ltd., Kyoto, Japan, was dissolved in 60 parts by weight of water, and the solution was heated to 65° C., adjusted to pH 5.5, and admixed with one unit/g reducing amylaceous saccharide, d.s.b., of a recombinant thermostable enzyme obtained by the method in Example A-1, followed by the enzymatic reaction for 96 hours. The reaction mixture was heated at 97° C. for 30 min to inactivate the remaining enzyme, diluted up to a concentration of about 20 w/w %, d.s.b., and admixed with 10 units/g reducing amylaceous saccharide, d.s.b., of "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, followed by the enzymatic reaction for 40 hours. Thereafter, the reaction mixture was heated to inactivate the remaining enzyme, cooled, filtered, and, in usual manner, decolorized with an activated charcoal, desalted and purified with an ion exchanger, and concentrated into an about 60 w/w % solution. The concentrate with a trehalose content of 30.1 w/w %, d.s.b., was subjected to column chromatographic fractionation similarly as in Example B-2 except that "CG6000", a strong-acid cation exchange resin in Na<sup>+</sup>-form commercialized by Japan Organo Co., Ltd., Tokyo, Japan, was used to obtain a fraction containing about 97 w/w % trehalose, d.s.b.

The fraction was concentrated up to about 75 w/w %, d.s.b., transferred to a crystallizer, and gradually cooled while stirring to obtain a masseccite with a crystallization percentage of about 45 w/w %, d.s.b. The masseccite was sprayed downward from a nozzle equipped on the upper part of a spraying tower at a pressure of about 150 kg/cm<sup>2</sup> while an about 85° C. hot air was blowing downward from the upper part of the spraying tower, and the formed crystalline powder was collected on a wire-netting conveyer provided on the basement of the drying tower and gradually conveyed out of the spraying tower while an about 45° C. hot air was blowing to the crystalline powder from under the conveyer. The crystalline powder thus obtained was transferred to an ageing tower and aged for 10 hours in a hot air stream to complete the crystallization and drying. Thus, a powdery hydrous crystalline trehalose was obtained in a yield of about 90 w/w % to the material, d.s.b.

The product having substantial no hygroscopicity and satisfactory handleability can be suitably incorporated into compositions in general such as food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient, and adjuvant.

#### EXAMPLE B-6

##### Conversion into Syrupy Product Containing Non-Reducing Saccharide

A high-purity maltotetraose commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was dissolved in water into a 40 w/w % aqueous solution which was then mixed with 2.0 units/g maltotetraose, d.s.b., of a

recombinant thermostable enzyme obtained by the method in Example A-2, and subjected to an enzymatic reaction at 60° C. for 72 hours to obtain a reaction mixture containing about 57 w/w %  $\alpha$ -maltosyltrehalose and about 9 w/w %  $\alpha$ -glucosyltrehalose, d.s.b. The reaction mixture was incubated at 97° C. for 30 min to inactivate the remaining enzyme, cooled, filtered in usual manner, decolorized with an activated charcoal, deionized and purified with an ion exchanger, and concentrated.

The resultant concentrate was fed to a column in Example B-2, and fractions rich in  $\alpha$ -maltosyltrehalose were collected, purified in usual manner, and concentrated to obtain an about 70 w/w % syrupy product in a yield of about 90% to the material maltotetraose, d.s.b.

The product with a low DE of 3.7, 84 w/w %  $\alpha$ -maltosyltrehalose and 4.0 w/w %  $\alpha$ -glucosyltrehalose, d.s.b., has a mild and high-quality sweetness and an adequate viscosity and moisture-retaining ability, and can be arbitrarily used as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and diluent in compositions in general such as food products, cosmetics and pharmaceuticals.

As is described above, the present invention is based on the finding of a novel thermostable enzyme which forms non-reducing saccharides having a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3. The present invention is to explore a way to produce such a thermostable enzyme in an industrial scale and in a relatively-high efficiency by the recombinant DNA technology. The present conversion method using the recombinant thermostable enzyme readily converts non-reducing amylaceous saccharides, having a degree of glucose polymerization of at least 3, into non-reducing saccharides having a trehalose structure as an end unit without fear of causing bacterial contamination. The non-reducing saccharides have a mild and high-quality sweetness, and, because they have no reducing residue within their molecules, they can be advantageously incorporated into compositions in general such as food products, cosmetics and pharmaceuticals without fear of causing unsatisfactory coloration and deterioration. The present recombinant thermostable enzyme is the one with a revealed amino acid sequence, so that it can be used freely in the preparations of non-reducing saccharides having a trehalose structure as an end unit which are premised to be used in food products and pharmaceuticals.

Thus, the present invention is a significant invention which exerts the aforesaid satisfactory effects and greatly contributes to this field.

While there has been described what is at present considered to be the preferred embodiments of the invention, it will be understood that various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirit and scope of the invention.

#### SEQUENCE LISTING

##### (1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 19

-continued

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val	Ile	Ser	Ala	Thr	Tyr	Arg	Leu	Gln	Leu	Asn	Lys	Asn	Phe	Asn	Phe	1	5	10	15
Gly	Asp	Val	Ile	Asp	Asn	Leu	Trp	Tyr	Phe	Lys	Asp	Leu	Gly	Val	Ser	20	25	30	
His	Leu	Tyr	Leu	Ser	Pro	Val	Leu	Met	Ala	Ser	Pro	Gly	Ser	Asn	His	35	40	45	
Gly	Tyr	Asp	Val	Ile	Asp	His	Ser	Arg	Ile	Asn	Asp	Glu	Leu	Gly	Gly	50	55	60	
Glu	Lys	Glu	Tyr	Arg	Arg	Leu	Ile	Glu	Thr	Ala	His	Thr	Ile	Gly	Leu	65	70	75	80
Gly	Ile	Ile	Gln	Asp	Ile	Val	Pro	Asn	His	Met	Ala	Val	Asn	Ser	Leu	85	90	95	
Asn	Trp	Arg	Leu	Met	Asp	Val	Leu	Lys	Met	Gly	Lys	Lys	Ser	Lys	Tyr	100	105	110	
Tyr	Thr	Tyr	Phe	Asp	Phe	Phe	Pro	Glu	Asp	Asp	Lys	Ile	Arg	Leu	Pro	115	120	125	
Ile	Leu	Gly	Glu	Asp	Leu	Asp	Thr	Val	Ile	Ser	Lys	Gly	Leu	Leu	Lys	130	135	140	
Ile	Val	Lys	Asp	Gly	Asp	Glu	Tyr	Phe	Leu	Glu	Tyr	Phe	Lys	Trp	Lys	145	150	155	160
Leu	Pro	Leu	Thr	Glu	Val	Gly	Asn	Asp	Ile	Tyr	Asp	Thr	Leu	Gln	Lys	165	170	175	
Gln	Asn	Tyr	Thr	Leu	Met	Ser	Trp	Lys	Asn	Pro	Pro	Ser	Tyr	Arg	Arg	180	185	190	
Phe	Phe	Asp	Val	Asn	Thr	Leu	Ile	Gly	Val	Asn	Val	Glu	Lys	Asp	His	195	200	205	
Val	Phe	Gln	Glu	Ser	His	Ser	Lys	Ile	Leu	Asp	Leu	Asp	Val	Asp	Gly	210	215	220	
Tyr	Arg	Ile	Asp	His	Ile	Asp	Gly	Leu	Tyr	Asp	Pro	Glu	Lys	Tyr	Ile	225	230	235	240
Asn	Asp	Leu	Arg	Ser	Ile	Ile	Lys	Asn	Lys	Ile	Ile	Ile	Val	Glu	Lys	245	250	255	
Ile	Leu	Gly	Phe	Gln	Glu	Glu	Leu	Lys	Leu	Asn	Ser	Asp	Gly	Thr	Thr	260	265	270	
Gly	Tyr	Asp	Phe	Leu	Asn	Tyr	Ser	Asn	Leu	Leu	Phe	Asn	Phe	Asn	Gln	275	280	285	
Glu	Ile	Met	Asp	Ser	Ile	Tyr	Glu	Asn	Phe	Thr	Ala	Glu	Lys	Ile	Ser	290	295	300	
Ile	Ser	Glu	Ser	Ile	Lys	Lys	Ile	Lys	Ala	Gln	Ile	Ile	Asp	Glu	Leu	305	310	315	320
Phe	Ser	Tyr	Glu	Val	Lys	Arg	Leu	Ala	Ser	Gln	Leu	Gly	Ile	Ser	Tyr	325	330	335	
Asp	Ile	Leu	Arg	Asp	Tyr	Leu	Ser	Cys	Ile	Asp	Val	Tyr	Arg	Thr	Tyr	340	345	350	
Ala	Asn	Gln	Ile	Val	Lys	Glu	Cys	Asp	Lys	Thr	Asn	Glu	Ile	Glu	Glu	355	360	365	

-continued

Ala	Thr	Lys	Arg	Asn	Pro	Glu	Ala	Tyr	Thr	Lys	Leu	Gln	Gln	Tyr	Met
370						375					380				
Pro	Ala	Val	Tyr	Ala	Lys	Ala	Tyr	Glu	Asp	Thr	Phe	Leu	Phe	Arg	Tyr
385					390					395					400
Asn	Arg	Leu	Ile	Ser	Ile	Asn	Glu	Val	Gly	Ser	Asp	Leu	Arg	Tyr	Tyr
			405						410					415	
Lys	Ile	Ser	Pro	Asp	Gln	Phe	His	Val	Phe	Asn	Gln	Lys	Arg	Arg	Gly
			420					425					430		
Lys	Ile	Thr	Leu	Asn	Ala	Thr	Ser	Thr	His	Asp	Thr	Lys	Phe	Ser	Glu
		435					440					445			
Asp	Val	Arg	Met	Lys	Ile	Ser	Val	Leu	Ser	Glu	Phe	Pro	Glu	Glu	Trp
	450					455					460				
Lys	Asn	Lys	Val	Glu	Glu	Trp	His	Ser	Ile	Ile	Asn	Pro	Lys	Val	Ser
465					470					475					480
Arg	Asn	Asp	Glu	Tyr	Arg	Tyr	Tyr	Gln	Val	Leu	Val	Gly	Ser	Phe	Tyr
			485						490					495	
Glu	Gly	Phe	Ser	Asn	Asp	Phe	Lys	Glu	Arg	Ile	Lys	Gln	His	Met	Ile
			500					505					510		
Lys	Ser	Val	Arg	Glu	Ala	Lys	Ile	Asn	Thr	Ser	Trp	Arg	Asn	Gln	Asn
		515					520					525			
Lys	Glu	Tyr	Glu	Asn	Arg	Val	Met	Glu	Leu	Val	Glu	Glu	Thr	Phe	Thr
	530					535					540				
Asn	Lys	Asp	Phe	Ile	Lys	Ser	Phe	Met	Lys	Phe	Glu	Ser	Lys	Ile	Arg
545					550					555					560
Arg	Ile	Gly	Met	Ile	Lys	Ser	Leu	Ser	Leu	Val	Ala	Leu	Lys	Ile	Met
			565						570					575	
Ser	Ala	Gly	Ile	Pro	Asp	Phe	Tyr	Gln	Gly	Thr	Glu	Ile	Trp	Arg	Tyr
		580						585					590		
Leu	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Val	Pro	Val	Asp	Phe	Lys	Lys	Leu
		595					600					605			
His	Glu	Ile	Leu	Glu	Lys	Ser	Lys	Lys	Phe	Glu	Lys	Asn	Met	Leu	Glu
	610					615					620				
Ser	Met	Asp	Asp	Gly	Arg	Ile	Lys	Met	Tyr	Leu	Thr	Tyr	Lys	Leu	Leu
625					630					635					640
Ser	Leu	Arg	Lys	Gln	Leu	Ala	Glu	Asp	Phe	Leu	Lys	Gly	Glu	Tyr	Lys
			645						650					655	
Gly	Leu	Asp	Leu	Glu	Glu	Gly	Leu	Cys	Gly	Phe	Ile	Arg	Phe	Asn	Lys
		660						665					670		
Ile	Leu	Val	Ile	Ile	Lys	Thr	Lys	Gly	Ser	Val	Asn	Tyr	Lys	Leu	Lys
		675					680					685			
Leu	Glu	Glu	Gly	Ala	Ile	Tyr	Thr	Asp	Val	Leu	Thr	Gly	Glu	Glu	Ile
	690					695					700				
Lys	Lys	Glu	Val	Gln	Ile	Asn	Glu	Leu	Pro	Arg	Ile	Leu	Val	Arg	Met
705					710					715					720

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGATATCAG CAACCTACAG ATTACAGTTA AATAAGAATT TTAATTTTGG TGACGTAATC 60

-continued

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GATAACCTAT	GGTATTTTAA	GGATTTAGGA	GTTTCCCATC	TCTACCTCTC	TCCTGTCTTA	120
ATGGCTTCGC	CAGGAAGTAA	CCATGGGTAC	GATGTAATAG	ATCATTCAAG	GATAAACGAT	180
GAAC TTGGAG	GAGAGAAAAG	ATACAGGAGA	TTAATAGAGA	CAGCTCATAC	TATTGGATTA	240
GGTATTATAC	AGGACATAGT	ACCAAATCAC	ATGGCTGTAA	ATTCTCTAAA	TTGGCGACTA	300
ATGGATGTAT	TAAAAATGGG	TAAAAAGAGT	AAATATTATA	CGTACTTTGA	CTTTTCCCA	360
GAAGATGATA	AGATACGATT	ACCCATATTA	GGAGAAGATT	TAGATACAGT	GATAAGTAAA	420
GGTTTATTAA	AGATAGTAAA	AGATGGAGAT	GAATATTTCC	TAGAATATTT	CAAATGGAAA	480
CTTCCTCTAA	CAGAGGTTGG	AAATGATATA	TACGACACTT	TACAAAAACA	GAATTATACC	540
CTAATGTCTT	GGAAAAATCC	TCCTAGCTAT	AGACGATTCT	TCGATGTTAA	TACTTTAATA	600
GGAGTAAATG	TCGAAAAAGA	TCACGTATTT	CAAGAGTCCC	ATTCAAAGAT	CTTAGATTTA	660
GATGTTGATG	GCTATAGAAT	TGATCATATT	GATGGATTAT	ATGATCCTGA	GAAATATATT	720
AATGACCTGA	GGTCAATAAT	TAAAAATAAA	ATAATTATTG	TAGAAAAAAT	TCTGGGATTT	780
CAGGAGGAAT	TAAAATTAAA	TTCAGATGGA	ACTACAGGAT	ATGACTTCTT	AAATTACTCC	840
AACTTACTGT	TTAATTTTAA	TCAAGAGATA	ATGGACAGTA	TATATGAGAA	TTTCACAGCG	900
GAGAAAATAT	CTATAAGTGA	AAGTATAAAG	AAAATAAAAG	CGCAAATAAT	TGATGAGCTA	960
TTTAGTTATG	AAGTTAAAAG	ATTAGCATCA	CAACTAGGAA	TTAGCTACGA	TATATTGAGA	1020
GATTACCTTT	CTTGTATAGA	TGTGTACAGA	ACTTATGCTA	ATCAGATTGT	AAAAGAGTGT	1080
GATAAGACCA	ATGAGATAGA	GGAAGCAACC	AAAAGAAATC	CAGAGGCTTA	TACTAAATTA	1140
CAACAATATA	TGCCAGCAGT	ATACGCTAAA	GCTTATGAAG	ATACTTTCCT	CTTTAGATAC	1200
AATAGATTAA	TATCCATAAA	TGAGGTTGGA	AGCGATTTAC	GATATTATAA	GATATCGCCT	1260
GATCAGTTTC	ATGTATTTAA	TCAAAAACGA	AGAGGAAAAA	TCACACTAAA	TGCCACTAGC	1320
ACACATGATA	CTAAGTTTAG	TGAAGATGTA	AGGATGAAAA	TAAGTGATT	AAGTGAATTT	1380
CCTGAAGAAT	GGAAAAATAA	GGTCGAGGAA	TGGCATAGTA	TCATAAATCC	AAAGGTATCA	1440
AGAAATGATG	AATATAGATA	TTATCAGGTT	TTAGTGGGAA	GTTTTTATGA	GGGATTCTCT	1500
AATGATTTTA	AGGAGAGAAT	AAAGCAACAT	ATGATAAAAA	GTGTCAGAGA	AGCTAAGATA	1560
AATACCTCAT	GGAGAAATCA	AAATAAAGAA	TATGAAAATA	GAGTAATGGA	ATTAGTGGA	1620
GAAACTTTTA	CCAATAAGGA	TTTCATTAAA	AGTTTCATGA	AATTTGAAAG	TAAGATAAGA	1680
AGGATAGGGA	TGATTAAGAG	CTTATCCTTG	GTCGCATTAA	AAATTATGTC	AGCCGGTATA	1740
CCTGATTTTT	ATCAGGGAAC	AGAAATATGG	CGATATTTAC	TTACAGATCC	AGATAACAGA	1800
GTCCCAGTGG	ATTTTAAGAA	ATTACACGAA	ATATTAGAAA	AATCCAAAAA	ATTTGAAAAA	1860
AATATGTTAG	AGTCTATGGA	CGATGGAAGA	ATTAAGATGT	ATTTAACATA	TAAGCTTTTA	1920
TCCCTAAGAA	AACAGTTGGC	TGAGGATTTT	TTAAAGGGCG	AGTATAAGGG	ATTAGATCTA	1980
GAAGAAGGAC	TATGTGGGTT	TATTAGGTTT	AACAAAATTT	TGGTAATAAT	AAAAACCAAG	2040
GGAAGTGTTA	ATTACAAACT	GAAACTTGAA	GAGGGAGCAA	TTTACACAGA	TGTATTGACA	2100
GGAGAAGAAA	TTAAAAAAGA	GGTACAGATT	AATGAGCTAC	CTAGGATACT	AGTTAGAATG	2160

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

-continued

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ile Ser Ala Thr Tyr Arg Leu Gln Leu Asn Lys Asn Phe Asn Phe  
 1 5 10 15

Gly Asp Val Ile Asp Asn Leu Trp Tyr Phe Lys Asp Leu Gly  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Glu Glu Trp His Ser Ile Ile Asn Pro Lys  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTG ATA TCA GCA ACC TAC AGA TTA CAG TTA AAT AAG AAT TTT AAT TTT 48  
 Val Ile Ser Ala Thr Tyr Arg Leu Gln Leu Asn Lys Asn Phe Asn Phe  
 1 5 10 15

GGT GAC GTA ATC GAT AAC CTA TGG TAT TTT AAG GAT TTA GGA GTT TCC 96  
 Gly Asp Val Ile Asp Asn Leu Trp Tyr Phe Lys Asp Leu Gly Val Ser  
 20 25 30

CAT CTC TAC CTC TCT CCT GTC TTA ATG GCT TCG CCA GGA AGT AAC CAT 144  
 His Leu Tyr Leu Ser Pro Val Leu Met Ala Ser Pro Gly Ser Asn His  
 35 40 45

GGG TAC GAT GTA ATA GAT CAT TCA AGG ATA AAC GAT GAA CTT GGA GGA 192  
 Gly Tyr Asp Val Ile Asp His Ser Arg Ile Asn Asp Glu Leu Gly Gly  
 50 55 60

GAG AAA GAA TAC AGG AGA TTA ATA GAG ACA GCT CAT ACT ATT GGA TTA 240  
 Glu Lys Glu Tyr Arg Arg Leu Ile Glu Thr Ala His Thr Ile Gly Leu  
 65 70 75 80

GGT ATT ATA CAG GAC ATA GTA CCA AAT CAC ATG GCT GTA AAT TCT CTA 288  
 Gly Ile Ile Gln Asp Ile Val Pro Asn His Met Ala Val Asn Ser Leu  
 85 90 95

AAT TGG CGA CTA ATG GAT GTA TTA AAA ATG GGT AAA AAG AGT AAA TAT 336  
 Asn Trp Arg Leu Met Asp Val Leu Lys Met Gly Lys Lys Ser Lys Tyr  
 100 105 110

TAT ACG TAC TTT GAC TTT TTC CCA GAA GAT GAT AAG ATA CGA TTA CCC 384  
 Tyr Thr Tyr Phe Asp Phe Phe Pro Glu Asp Asp Lys Ile Arg Leu Pro  
 115 120 125

ATA TTA GGA GAA GAT TTA GAT ACA GTG ATA AGT AAA GGT TTA TTA AAG 432  
 Ile Leu Gly Glu Asp Leu Asp Thr Val Ile Ser Lys Gly Leu Leu Lys  
 130 135 140

ATA GTA AAA GAT GGA GAT GAA TAT TTC CTA GAA TAT TTC AAA TGG AAA 480  
 Ile Val Lys Asp Gly Asp Glu Tyr Phe Leu Glu Tyr Phe Lys Trp Lys  
 145 150 155 160

CTT CCT CTA ACA GAG GTT GGA AAT GAT ATA TAC GAC ACT TTA CAA AAA 528

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Leu	Pro	Leu	Thr	Glu	Val	Gly	Asn	Asp	Ile	Tyr	Asp	Thr	Leu	Gln	Lys	
				165					170					175		
CAG	AAT	TAT	ACC	CTA	ATG	TCT	TGG	AAA	AAT	CCT	CCT	AGC	TAT	AGA	CGA	576
Gln	Asn	Tyr	Thr	Leu	Met	Ser	Trp	Lys	Asn	Pro	Pro	Ser	Tyr	Arg	Arg	
			180					185					190			
TTC	TTC	GAT	GTT	AAT	ACT	TTA	ATA	GGA	GTA	AAT	GTC	GAA	AAA	GAT	CAC	624
Phe	Phe	Asp	Val	Asn	Thr	Leu	Ile	Gly	Val	Asn	Val	Glu	Lys	Asp	His	
		195					200					205				
GTA	TTT	CAA	GAG	TCC	CAT	TCA	AAG	ATC	TTA	GAT	TTA	GAT	GTT	GAT	GGC	672
Val	Phe	Gln	Glu	Ser	His	Ser	Lys	Ile	Leu	Asp	Leu	Asp	Val	Asp	Gly	
	210					215					220					
TAT	AGA	ATT	GAT	CAT	ATT	GAT	GGA	TTA	TAT	GAT	CCT	GAG	AAA	TAT	ATT	720
Tyr	Arg	Ile	Asp	His	Ile	Asp	Gly	Leu	Tyr	Asp	Pro	Glu	Lys	Tyr	Ile	
225					230					235					240	
AAT	GAC	CTG	AGG	TCA	ATA	ATT	AAA	AAT	AAA	ATA	ATT	ATT	GTA	GAA	AAA	768
Asn	Asp	Leu	Arg	Ser	Ile	Ile	Lys	Asn	Lys	Ile	Ile	Ile	Val	Glu	Lys	
				245				250						255		
ATT	CTG	GGA	TTT	CAG	GAG	GAA	TTA	AAA	TTA	AAT	TCA	GAT	GGA	ACT	ACA	816
Ile	Leu	Gly	Phe	Gln	Glu	Glu	Leu	Lys	Leu	Asn	Ser	Asp	Gly	Thr	Thr	
			260					265					270			
GGA	TAT	GAC	TTC	TTA	AAT	TAC	TCC	AAC	TTA	CTG	TTT	AAT	TTT	AAT	CAA	864
Gly	Tyr	Asp	Phe	Leu	Asn	Tyr	Ser	Asn	Leu	Leu	Phe	Asn	Phe	Asn	Gln	
		275					280					285				
GAG	ATA	ATG	GAC	AGT	ATA	TAT	GAG	AAT	TTC	ACA	GCG	GAG	AAA	ATA	TCT	912
Glu	Ile	Met	Asp	Ser	Ile	Tyr	Glu	Asn	Phe	Thr	Ala	Glu	Lys	Ile	Ser	
	290					295					300					
ATA	AGT	GAA	AGT	ATA	AAG	AAA	ATA	AAA	GCG	CAA	ATA	ATT	GAT	GAG	CTA	960
Ile	Ser	Glu	Ser	Ile	Lys	Lys	Ile	Lys	Ala	Gln	Ile	Ile	Asp	Glu	Leu	
305					310					315					320	
TTT	AGT	TAT	GAA	GTT	AAA	AGA	TTA	GCA	TCA	CAA	CTA	GGA	ATT	AGC	TAC	1008
Phe	Ser	Tyr	Glu	Val	Lys	Arg	Leu	Ala	Ser	Gln	Leu	Gly	Ile	Ser	Tyr	
				325				330						335		
GAT	ATA	TTG	AGA	GAT	TAC	CTT	TCT	TGT	ATA	GAT	GTG	TAC	AGA	ACT	TAT	1056
Asp	Ile	Leu	Arg	Asp	Tyr	Leu	Ser	Cys	Ile	Asp	Val	Tyr	Arg	Thr	Tyr	
			340					345					350			
GCT	AAT	CAG	ATT	GTA	AAA	GAG	TGT	GAT	AAG	ACC	AAT	GAG	ATA	GAG	GAA	1104
Ala	Asn	Gln	Ile	Val	Lys	Glu	Cys	Asp	Lys	Thr	Asn	Glu	Ile	Glu	Glu	
		355					360					365				
GCA	ACC	AAA	AGA	AAT	CCA	GAG	GCT	TAT	ACT	AAA	TTA	CAA	CAA	TAT	ATG	1152
Ala	Thr	Lys	Arg	Asn	Pro	Glu	Ala	Tyr	Thr	Lys	Leu	Gln	Gln	Tyr	Met	
		370				375						380				
CCA	GCA	GTA	TAC	GCT	AAA	GCT	TAT	GAA	GAT	ACT	TTC	CTC	TTT	AGA	TAC	1200
Pro	Ala	Val	Tyr	Ala	Lys	Ala	Tyr	Glu	Asp	Thr	Phe	Leu	Phe	Arg	Tyr	
					390					395					400	
AAT	AGA	TTA	ATA	TCC	ATA	AAT	GAG	GTT	GGA	AGC	GAT	TTA	CGA	TAT	TAT	1248
Asn	Arg	Leu	Ile	Ser	Ile	Asn	Glu	Val	Gly	Ser	Asp	Leu	Arg	Tyr	Tyr	
				405				410						415		
AAG	ATA	TCG	CCT	GAT	CAG	TTT	CAT	GTA	TTT	AAT	CAA	AAA	CGA	AGA	GGA	1296
Lys	Ile	Ser	Pro	Asp	Gln	Phe	His	Val	Phe	Asn	Gln	Lys	Arg	Arg	Gly	
			420					425					430			
AAA	ATC	ACA	CTA	AAT	GCC	ACT	AGC	ACA	CAT	GAT	ACT	AAG	TTT	AGT	GAA	1344
Lys	Ile	Thr	Leu	Asn	Ala	Thr	Ser	Thr	His	Asp	Thr	Lys	Phe	Ser	Glu	
		435					440					445				
GAT	GTA	AGG	ATG	AAA	ATA	AGT	GTA	TTA	AGT	GAA	TTT	CCT	GAA	GAA	TGG	1392
Asp	Val	Arg	Met	Lys	Ile	Ser	Val	Leu	Ser	Glu	Phe	Pro	Glu	Glu	Trp	
		450				455						460				
AAA	AAT	AAG	GTC	GAG	GAA	TGG	CAT	AGT	ATC	ATA	AAT	CCA	AAG	GTA	TCA	1440
Lys	Asn	Lys	Val	Glu	Glu	Trp	His	Ser	Ile	Ile	Asn	Pro	Lys	Val	Ser	
					470					475					480	
AGA	AAT	GAT	GAA	TAT	AGA	TAT	TAT	CAG	GTT	TTA	GTG	GGA	AGT	TTT	TAT	1488

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Arg	Asn	Asp	Glu	Tyr	Arg	Tyr	Tyr	Gln	Val	Leu	Val	Gly	Ser	Phe	Tyr	
				485					490					495		
GAG	GGA	TTC	TCT	AAT	GAT	TTT	AAG	GAG	AGA	ATA	AAG	CAA	CAT	ATG	ATA	1536
Glu	Gly	Phe	Ser	Asn	Asp	Phe	Lys	Glu	Arg	Ile	Lys	Gln	His	Met	Ile	
			500					505					510			
AAA	AGT	GTC	AGA	GAA	GCT	AAG	ATA	AAT	ACC	TCA	TGG	AGA	AAT	CAA	AAT	1584
Lys	Ser	Val	Arg	Glu	Ala	Lys	Ile	Asn	Thr	Ser	Trp	Arg	Asn	Gln	Asn	
		515					520					525				
AAA	GAA	TAT	GAA	AAT	AGA	GTA	ATG	GAA	TTA	GTG	GAA	GAA	ACT	TTT	ACC	1632
Lys	Glu	Tyr	Glu	Asn	Arg	Val	Met	Glu	Leu	Val	Glu	Glu	Thr	Phe	Thr	
		530				535					540					
AAT	AAG	GAT	TTC	ATT	AAA	AGT	TTC	ATG	AAA	TTT	GAA	AGT	AAG	ATA	AGA	1680
Asn	Lys	Asp	Phe	Ile	Lys	Ser	Phe	Met	Lys	Phe	Glu	Ser	Lys	Ile	Arg	
545					550					555					560	
AGG	ATA	GGG	ATG	ATT	AAG	AGC	TTA	TCC	TTG	GTC	GCA	TTA	AAA	ATT	ATG	1728
Arg	Ile	Gly	Met	Ile	Lys	Ser	Leu	Ser	Leu	Val	Ala	Leu	Lys	Ile	Met	
				565					570					575		
TCA	GCC	GGT	ATA	CCT	GAT	TTT	TAT	CAG	GGA	ACA	GAA	ATA	TGG	CGA	TAT	1776
Ser	Ala	Gly	Ile	Pro	Asp	Phe	Tyr	Gln	Gly	Thr	Glu	Ile	Trp	Arg	Tyr	
			580					585					590			
TTA	CTT	ACA	GAT	CCA	GAT	AAC	AGA	GTC	CCA	GTG	GAT	TTT	AAG	AAA	TTA	1824
Leu	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Val	Pro	Val	Asp	Phe	Lys	Lys	Leu	
		595				600						605				
CAC	GAA	ATA	TTA	GAA	AAA	TCC	AAA	AAA	TTT	GAA	AAA	AAT	ATG	TTA	GAG	1872
His	Glu	Ile	Leu	Glu	Lys	Ser	Lys	Lys	Phe	Glu	Lys	Asn	Met	Leu	Glu	
		610				615					620					
TCT	ATG	GAC	GAT	GGA	AGA	ATT	AAG	ATG	TAT	TTA	ACA	TAT	AAG	CTT	TTA	1920
Ser	Met	Asp	Asp	Gly	Arg	Ile	Lys	Met	Tyr	Leu	Thr	Tyr	Lys	Leu	Leu	
					630					635					640	
TCC	CTA	AGA	AAA	CAG	TTG	GCT	GAG	GAT	TTT	TTA	AAG	GGC	GAG	TAT	AAG	1968
Ser	Leu	Arg	Lys	Gln	Leu	Ala	Glu	Asp	Phe	Leu	Lys	Gly	Glu	Tyr	Lys	
				645					650					655		
GGA	TTA	GAT	CTA	GAA	GAA	GGA	CTA	TGT	GGG	TTT	ATT	AGG	TTT	AAC	AAA	2016
Gly	Leu	Asp	Leu	Glu	Glu	Gly	Leu	Cys	Gly	Phe	Ile	Arg	Phe	Asn	Lys	
			660					665					670			
ATT	TTG	GTA	ATA	ATA	AAA	ACC	AAG	GGA	AGT	GTT	AAT	TAC	AAA	CTG	AAA	2064
Ile	Leu	Val	Ile	Ile	Lys	Thr	Lys	Gly	Ser	Val	Asn	Tyr	Lys	Leu	Lys	
			675				680					685				
CTT	GAA	GAG	GGA	GCA	ATT	TAC	ACA	GAT	GTA	TTG	ACA	GGA	GAA	GAA	ATT	2112
Leu	Glu	Glu	Gly	Ala	Ile	Tyr	Thr	Asp	Val	Leu	Thr	Gly	Glu	Glu	Ile	
			690				695				700					
AAA	AAA	GAG	GTA	CAG	ATT	AAT	GAG	CTA	CCT	AGG	ATA	CTA	GTT	AGA	ATG	2160
Lys	Lys	Glu	Val	Gln	Ile	Asn	Glu	Leu	Pro	Arg	Ile	Leu	Val	Arg	Met	
					710					715					720	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCCGTTCT	GGCAAATATT	CTGAAATGAG	CTGTTGACAA	TTAATCATCG	GCTCGTCTAA	60
TGTGTGGAAT	TCTGATTCGA	ATTTTTTAAT	AAAATCAGGA	GGAAAAATA	TGATATCAGC	120
AACCTACAGA	TTACAGTTAA	ATAAGAATTT	TAATTTTGGT	GACGTAATCG	ATGAATTCAC	180
TAGTTAGAAT	GTGATGAAGG	CCTGCGGCCG	CTGCAGAGCT	CA		222



## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAYYTNTGGT AYT TYAARGA

20

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GARGARTGGC AYWSNATHAT

20

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCCGTTCT GGCAAATATT CTGAAATGAG CTGT

34

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGACAATTAA TCATCGGCTC GTCTAATGTG TGAATTCTG ATTCGA

46

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTTTTTAAT AAAATCAGGA GGAAAAAATA TGATATCAGC AACCTACA

48

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATTACAGTT AAATAAGAAT TTTAATTTTG GTGACGTAAT CGATGAA 47

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCAC TAGTT AGAATGTGAT GAAGGCCTGC GGCCGCTGCA GAGCTCA 47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGATGATTAA TTGTCAACAG CTCATTTTCAG AATATTTGCC AGAAGC 46

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTATTAAA AAATTCGAAT CAGAATTCCA CACATTAGAC GAGC 44

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTAACTGTAA TCTGTAGGTT GCTGATATCA TATTTTTTCC TCCTGA 46

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
TAGTGAATTC TACGATTACG TCACCAAAAT TAAAATTCTT AT 42

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
AGCTTGAGCT CTGCAGCGGC CGCAGGCCTT CATCACATTC TAAC 44

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
GTAAAACGAC GGCCAGT 17

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We claim:

1. A method for converting a reducing amylaceous saccharide to form a non-reducing saccharide having a trehalose structure as an end unit, comprising the steps of:

transforming a host microorganism with a recombinant DNA molecule encoding a thermostable enzyme, which forms a non-reducing saccharide having a trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher, to obtain a recombinant microorganism, wherein the thermostable enzyme has an amino acid sequence selected from the group consisting of SEQ ID NO:1 and functional variants thereof in which one amino acid residue in SEQ ID NO:1 is replaced with a different amino acid or deleted, or one or more amino acids are added to the N-terminus of SEQ ID NO:1, without substantially losing the physicochemical properties of said enzyme, which physicochemical properties include the following:

(1) Action

Forming non-reducing saccharides, having a trehalose structure as an end unit and a degree of polymerization of at least 3 from reducing amylaceous saccharides having a degree of glucose polymerization of at least 3;

(2) Molecular weight

About 69,000–79,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and

(3) Thermostability

Substantially not inactivated even when incubated in an aqueous solution (pH 7.0) at 85° C. for 60 min; culturing the recombinant microorganism to express and produce the enzyme; recovering the produced enzyme; and

subjecting a reducing amylaceous saccharide having a degree of glucose polymerization of at least 3 to the action of the recovered enzyme to convert the reducing amylaceous saccharide and form a non-reducing saccharide having a trehalose structure as an end unit and a degree of glucose polymerization of at least 3.

2. The method according to claim 1, wherein said reducing amylaceous saccharide is prepared by hydrogenating starch or amylaceous substance with an acid and/or an amylase.

3. The method according to claim 1, wherein said reducing amylaceous saccharide is selected from the group consisting of maltotriose, maltotetraose, maltopentaose, maltohexaose, maltoheptaose, and mixtures thereof.

4. The method according to claim 1, wherein said recombinant thermostable enzyme is allowed to coexist in an aqueous solution of said reducing amylaceous saccharide with a concentration of not higher than 50 w/w %, on a dry solid basis, and allowed to act on the reducing amylaceous saccharide at a temperature exceeding 55° C.

5. The method according to claim 1, wherein said non-reducing saccharide is selected from the group consisting of  $\alpha$ -glucosyltrehalose,  $\alpha$ -maltosyltrehalose,  $\alpha$ -maltotriosyltrehalose,  $\alpha$ -maltotetraosyltrehalose,  $\alpha$ -maltopentaosyltrehalose, and mixtures thereof.

6. A method for converting a reducing amylaceous saccharide to form a non-reducing saccharide having a trehalose structure as an end unit, comprising the steps of:

transforming a host cell with a recombinant DNA molecule encoding a thermostable enzyme, which forms a non-reducing saccharide having a trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher, to obtain a recombinant microorganism, wherein the thermostable enzyme has the following physicochemical properties:

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- (1) Action  
Forming non-reducing saccharides, having a trehalose structure as an end unit and a degree of polymerization of at least 3 from reducing amy-  
laceous saccharides having a degree of glucose 5  
polymerization of at least 3;
- (2) Molecular weight  
About 69,000–79,000 daltons on sodium dodecyl  
sulfate polyacrylamide gel electrophoresis (SDS-  
PAGE); 10
- (3) Thermostability  
Substantially not inactivated even when incubated in  
an aqueous solution (pH 7.0) at 85° C. for 60 min;
- (4) Isoelectric point (pI)  
About 5.4–6.4 on isoelectrophoresis; and
- (5) Amino acid sequence  
An amino acid sequence which is not identical to the  
amino acid sequence of SEQ ID NO:1 but which

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- contains the amino acid sequences of SEQ ID  
NO:3 and SEQ ID NO:4
- culturing the recombinant microorganism to express and  
produce the enzyme;
- recovering the produced enzyme; and
- subjecting a reducing amylose saccharide having a  
degree of glucose polymerization of at least 3 to the  
action of the recovered enzyme to convert the reducing  
amylose saccharide and form a non-reducing sac-  
charide having a trehalose structure as an end unit and  
a degree of glucose polymerization of at least 3.
7. The method according to claim 1, wherein the recom-  
binant DNA molecule encoding the thermostable enzyme  
comprises the nucleotide sequence of SEQ ID NO:5.

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